

181 GTAKKNGGLYYMAPEHLNDVNAKE

QY 181 GTAKKNGTLYYMAPEHLNDVNAKPTKESDVYSFAVLWAI FANKEPYENAI CEQQLIMC 240

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Db      181 GTAKNGGTLYYMAPEHNDVNAKPTKSDVYSFAVVLMAIPANKPEYENAIICBOQLIMC 240
QY      241 IKSGNRPDVDDITECPREIISLMKLCWEANPEARPTPGIEEKRFPFLISQLEESVED 300
Db      241 IKSGNRPDVDDITECPREIISLMKLCWEANPEARPTPGIEEKRFPFLISQLEESVED 300
QY      301 VKSLKKEYSNENAVKRMQSLQDLCVAVPSSRSNSATEPGSLHSSQGLGMPVEESMFA 360
Db      301 VKSLKKEYSNENAVKRMQSLQDLCVAVPSSRSNSATEPGSLHSSQGLGMPVEESMFA 360
QY      361 PSLEHPOEENEPSSLOSKLODEANYHLVYGRMDRQTKQOPRONVAVNREERRRVSHDPF 420
Db      361 PSLEHPOEENEPSSLOSKLODEANYHLVYGRMDRQTKQOPRONVAVNREERRRVSHDPF 420
QY      421 AQRREYENFQNTGEGKGYSSAASHGNVHOPSGILTSOPQVLYXNNGLYSSHGFTRPDL 480
Db      421 AQRREYENFQNTGEGKGYSSAASHGNVHOPSGILTSOPQVLYXNNGLYSSHGFTRPDL 480
QY      481 PGTAGPRVWYRPIPSHMSLHNIIPVETNYLGNTPMPFSSLPPTDESIRKTYINSGTIG 540
Db      481 PGTAGPRVWYRPIPSHMSLHNIIPVETNYLGNTPMPFSSLPPTDESIRKTYINSGTIG 540
QY      541 IGAYNYMEIGTSSSLDSTNTNFKKEPAKYQALFDNTTSLTDKHLDPIRENLGKHMKN 600
Db      541 IGAYNYMEIGTSSSLDSTNTNFKKEPAKYQALFDNTTSLTDKHLDPIRENLGKHMKN 600
QY      601 CARLIGFTOSQIDELDHEDYERDGLKEKYOMLOKVMREGIKGATVGLAQLHQCRRID 660
Db      601 CARLIGFTOSQIDELDHEDYERDGLKEKYOMLOKVMREGIKGATVGLAQLHQCRRID 660
QY      661 LLSSLIYSON 671
Db      661 LLSSLIYSON 671

```

RESULT 2

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; US-09-758-003-2
; Sequence 2, Application US/09758003
; Patent No. US20020098522A1
; GENERAL INFORMATION:

```

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APPLICANT: BAICHWAL, VIJAY R

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HOANG, JIANNING
HSU, HAILING
GOEDEL, DAVID V

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TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
ASSAYS

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NUMBER OF SEQUENCES: 2

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CORRESPONDENCE ADDRESS:

```

```

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

```

```

STREET: 75 DENISE DRIVE

```

```

CITY: HILLSBOROUGH

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```

STATE: CALIFORNIA

```

```

COUNTRY: USA

```

```

ZIP: 94010

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COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk

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OPERATING SYSTEM: IBM PC compatible

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SOFTWARE: Patentin Release #1.0, Version #1.30

```

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CURRENT APPLICATION DATA:

```

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APPLICATION NUMBER: US/09/758,003

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FILING DATE: 09-Jan-2001

```

```

CLASSIFICATION: <Unknown>

```

```

PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: 09/132,118

```

```

FILING DATE: <Unknown>

```

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ATTORNEY/AGENT INFORMATION:

```

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NAME: OSMAN, RICHARD A.

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REGISTRATION NUMBER: 36,627

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REFERENCE/DOCKET NUMBER: T95-006-1

```

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TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-758-003-2

```

```

Query Match      100.0%; Score 3545; DB 10; Length 671;
Best Local Similarity 100.0%; Pred. No. 5,9e-234;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MOPDMSLVYIKKSSDFLESALDSGGGKYSLSCEHRTQGLMIMKYVKGPNCTIEHNEAL 60
Db      1 MOPDMSLVYIKKSSDFLESALDSGGGKYSLSCEHRTQGLMIMKYVKGPNCTIEHNEAL 60
QY      61 LEEAKMNRRLRSRVYKLLGVITIEGKYSLVMEYKEGNLMHVLKAEKSTPLSKGRITL 120
Db      61 LEEAKMNRRLRSRVYKLLGVITIEGKYSLVMEYKEGNLMHVLKAEKSTPLSKGRITL 120
QY      121 EIEGMCYLHGKGVYHKDLKEPNIIVDNDPHIKIADGLASFRKMSKLNNEHNELEREVD 180
Db      121 EIEGMCYLHGKGVYHKDLKEPNIIVDNDPHIKIADGLASFRKMSKLNNEHNELEREVD 180
QY      181 GTAKNGGTLYYMAPEHNDVNAKPTKSDVYSFAVVLMAIPANKPEYENAIICBOQLIMC 240
Db      181 GTAKNGGTLYYMAPEHNDVNAKPTKSDVYSFAVVLMAIPANKPEYENAIICBOQLIMC 240
QY      241 IKSGNRPDVDDITECPREIISLMKLCWEANPEARPTPGIEEKRFPFLISQLEESVED 300
Db      241 IKSGNRPDVDDITECPREIISLMKLCWEANPEARPTPGIEEKRFPFLISQLEESVED 300
QY      301 VKSLKKEYSNENAVKRMQSLQDLCVAVPSSRSNSATEPGSLHSSQGLGMPVEESMFA 360
Db      301 VKSLKKEYSNENAVKRMQSLQDLCVAVPSSRSNSATEPGSLHSSQGLGMPVEESMFA 360
QY      361 PSLEHPOEENEPSSLOSKLODEANYHLVYGRMDRQTKQOPRONVAVNREERRRVSHDPF 420
Db      361 PSLEHPOEENEPSSLOSKLODEANYHLVYGRMDRQTKQOPRONVAVNREERRRVSHDPF 420
QY      421 AQRREYENFQNTGEGKGYSSAASHGNVHOPSGILTSOPQVLYXNNGLYSSHGFTRPDL 480
Db      421 AQRREYENFQNTGEGKGYSSAASHGNVHOPSGILTSOPQVLYXNNGLYSSHGFTRPDL 480
QY      481 PGTAGPRVWYRPIPSHMSLHNIIPVETNYLGNTPMPFSSLPPTDESIRKTYINSGTIG 540
Db      481 PGTAGPRVWYRPIPSHMSLHNIIPVETNYLGNTPMPFSSLPPTDESIRKTYINSGTIG 540
QY      541 IGAYNYMEIGTSSSLDSTNTNFKKEPAKYQALFDNTTSLTDKHLDPIRENLGKHMKN 600
Db      541 IGAYNYMEIGTSSSLDSTNTNFKKEPAKYQALFDNTTSLTDKHLDPIRENLGKHMKN 600
QY      601 CARLIGFTOSQIDELDHEDYERDGLKEKYOMLOKVMREGIKGATVGLAQLHQCRRID 660
Db      601 CARLIGFTOSQIDELDHEDYERDGLKEKYOMLOKVMREGIKGATVGLAQLHQCRRID 660
QY      661 LLSSLIYSON 671
Db      661 LLSSLIYSON 671

```

RESULT 3

```

; US-09-862-027-29
; Sequence 29, Application US/09862027
; Patent No. US20020142428A1
; GENERAL INFORMATION:

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APPLICANT: Hodge, Martin R.

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TITLE OF INVENTION: No. US20020142428A1el Kinases and Uses Thereof

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FILE REFERENCE: 35800/234862

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CURRENT APPLICATION NUMBER: US/09/862,027

```

CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 671
TYPE: PR1
ORGANISM: Homo sapiens
US-09-862-027-29

Query Match 100.0%; Score 3545; DB 10; Length 671;
Best Local Similarity 100.0%; Pred. No. 5.9e-234;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MOPDMSLVNFKMSDDLESNAELDSGGFGKVSICFHTQGLMKTYYKGPNCIEHNEAL 60
DB 1 MOPDMSLVNFKMSDDLESNAELDSGGFGKVSICFHTQGLMKTYYKGPNCIEHNEAL 60
QY 61 LEEAKMMNRRLRHSRVYKLLGVITIEEGKYSIVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
DB 61 LEEAKMMNRRLRHSRVYKLLGVITIEEGKYSIVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
QY 121 EIEEGMCTYLGKGYIHKDLKPENLVNDPFIKTLADGLASFMMKSKLNNEEHNELEVD 180
DB 121 EIEEGMCTYLGKGYIHKDLKPENLVNDPFIKTLADGLASFMMKSKLNNEEHNELEVD 180
QY 181 GTAKKNGGTYLYMAPEHLNDVNAKPTKSDVYSFAVYLAIFANKPEYENAIICEQOLIMC 240
DB 181 GTAKKNGGTYLYMAPEHLNDVNAKPTKSDVYSFAVYLAIFANKPEYENAIICEQOLIMC 240
QY 241 IKSGNRPDVDITIEYCPRETIISLMKLCWEANPEARPTFGIEEKFREFYLSOLEEVEED 300
DB 241 IKSGNRPDVDITIEYCPRETIISLMKLCWEANPEARPTFGIEEKFREFYLSOLEEVEED 300
QY 301 VKSLKKEYSENNAVYKRMOSLOLDCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESMFA 360
DB 301 VKSLKKEYSENNAVYKRMOSLOLDCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESMFA 360
QY 361 PSLHEPOEENEPISLOSLQDEANVHLGSRMDROTQOOPRONVAYNREBERRRVSDPF 420
DB 361 PSLHEPOEENEPISLOSLQDEANVHLGSRMDROTQOOPRONVAYNREBERRRVSDPF 420
QY 421 AAOORPVNFONTGKGTGVYSSAASHGNAVHOPSGLSOPOVLYONNGLYSHGFGTRPLD 480
DB 421 AAOORPVNFONTGKGTGVYSSAASHGNAVHOPSGLSOPOVLYONNGLYSHGFGTRPLD 480
QY 481 PGTAGPRVWYRPIPSHMPSLHNIPEPTNYLGNTPTMPFSSLPPTDESIKYTIYNSTGIC 540
DB 481 PGTAGPRVWYRPIPSHMPSLHNIPEPTNYLGNTPTMPFSSLPPTDESIKYTIYNSTGIC 540
QY 541 IGAVNYMEIGTSSSLDSTNTNFKKEPAKQAIFPNTTSLDKHLDPRENLGKHWKN 600
DB 541 IGAVNYMEIGTSSSLDSTNTNFKKEPAKQAIFPNTTSLDKHLDPRENLGKHWKN 600
QY 601 CARLGTOSQIDPIDHYERDGLKEKYVMLOKWMVREGIKATVGLAOLAHQCSRID 660
DB 601 CARLGTOSQIDPIDHYERDGLKEKYVMLOKWMVREGIKATVGLAOLAHQCSRID 660
QY 661 LLSLLIVSON 671
DB 661 LLSLLIVSON 671
```

RESULT 4
US-09-862-027-30
Sequence 30, Application US/09862027
Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. US20020142428A1el kinases and Uses thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027

CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 656
TYPE: PR1
ORGANISM: Mus musculus
US-09-862-027-30

Query Match 68.4%; Score 2423.5; DB 10; Length 656;
Best Local Similarity 69.8%; Pred. No. 2.2e-157;
Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

```
QY 1 MOPDMSLVNFKMSDDLESNAELDSGGFGKVSICFHTQGLMKTYYKGPNCIEHNEAL 60
DB 1 MOPDMSLVNFKMSDDLESNAELDSGGFGKVSICFHTQGLMKTYYKGPNCIEHNEAL 60
QY 61 LEEAKMMNRRLRHSRVYKLLGVITIEEGKYSIVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
DB 61 LEEAKMMNRRLRHSRVYKLLGVITIEEGKYSIVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
QY 121 EIEEGMCTYLGKGYIHKDLKPENLVNDPFIKTLADGLASFMMKSKLNNEEHNELEVD 180
DB 121 EIEEGMCTYLGKGYIHKDLKPENLVNDPFIKTLADGLASFMMKSKLNNEEHNELEVD 180
QY 181 GTAKKNGGTYLYMAPEHLNDVNAKPTKSDVYSFAVYLAIFANKPEYENAIICEQOLIM 239
DB 181 GTAKKNGGTYLYMAPEHLNDVNAKPTKSDVYSFAVYLAIFANKPEYENAIICEQOLIM 239
QY 240 CTKSGNRPDVDITIEYCPRETIISLMKLCWEANPEARPTFGIEEKFREFYLSOLEEVEE 299
DB 240 CTKSGNRPDVDITIEYCPRETIISLMKLCWEANPEARPTFGIEEKFREFYLSOLEEVEE 299
QY 241 CTKSGNRPDVDITIEYCPRETIISLMKLCWEANPEARPTFGIEEKFREFYLSOLEEVEE 300
DB 241 CTKSGNRPDVDITIEYCPRETIISLMKLCWEANPEARPTFGIEEKFREFYLSOLEEVEE 300
QY 300 DVSLKKEYSENNAVYKRMOSLOLDCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESMFA 359
DB 301 DVSLKKEYSENNAVYKRMOSLOLDCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESMFA 358
QY 360 APSLEHPOEENEPISLOSLQDEANVHLGSRMDROTQOOPRONVAYNREBERRRVSDPF 419
DB 359 APSLEHPOEENEPISLOSLQDEANVHLGSRMDROTQOOPRONVAYNREBERRRVSDPF 418
QY 420 FAOORPVNFONTGKGTGVYSSAASHGNAVHOPSGLSOPOVLYONNGLYSHGFGTRPL 479
DB 419 FAOORPVNFONTGKGTGVYSSAASHGNAVHOPSGLSOPOVLYONNGLYSHGFGTRPL 470
QY 480 DPGTAGPRVWYRPIPSHMPSLHNIPEPTNYLGNTPTMPFSSLPPTDESIKYTIYNSTGIC 539
DB 471 DPGTAGPRVWYRPIPSHMPSLHNIPEPTNYLGNTPTMPFSSLPPTDESIKYTIYNSTGIC 528
QY 540 QIGAVNYMEIGTSSSLDSTNTNFKKEPAKQAIFPNTTSLDKHLDPRENLGKHWKN 599
DB 529 QIGAVNYMEIGTSSSLDSTNTNFKKEPAKQAIFPNTTSLDKHLDPRENLGKHWKN 584
QY 600 NCARKLGTOSQIDPIDHYERDGLKEKYVMLOKWMVREGIKATVGLAOLAHQCSRID 659
DB 585 NCARKLGTOSQIDPIDHYERDGLKEKYVMLOKWMVREGIKATVGLAOLAHQCSRID 644
QY 660 LLSLLIVSON 671
DB 645 LLSLLIVSON 656
```

RESULT 5
US-09-862-027-8
Sequence 8, Application US/09862027
Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. US20020142428A1el kinases and Uses thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027

```

; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/345,473
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 497
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-862-027-8

```

```

Query Match      12.1%; Score 428; DB 10; Length 497;
Best Local Similarity 25.4%; Pred. No. 2,7e-21;
Matches 144; Conservative 95; Mismatches 182; Indels 146; Gaps 22;

```

```

OY 19 ESAL-DSGGFGVSLCFHRTGGLMTKTVYKPCNIEHNEALLBEAKMNLRLRSRYK 77
DB 1 ENQELVKGKGGFTVFAOHRKMG-----YVAVKIVNSKAIISREVKAMASLDNEFVLK 53
OY 78 LAGVI-----IEGKYSLYMEYKGNLMHVLKAEKSTPLSVKGRILEIEIGMCYLHGK 132
DB 54 LEGVIEKVMWDDPKPALVTKFMENGLSGLLQSCPRPWLICRLKKEVVLGMFYLDQ 113
OY 133 G--VIHKDKPENILVNDNFIKIADLGLASFRRMMSKLNNEHNEELREVDTAK-KNGGT 189
DB 114 NPVLLHRDLKPSNVLPDPDLHVKLADFGISTFGGSG-----SGTSGEGPGT 161
OY 190 LYMAPEHLNDVNAKPTKSDVYSFAVYVIMAFANKE---PYE-----NAICEQOLMCI 241
DB 162 LGYLAPELVFNVRRASTASDVYSFGILMAYLAEREVELPEPSLYEAVCNRQ----- 216
OY 242 KGNRPDDVDITEYCPRE-----ITSLMKLCWEANPEARPTP---PGIEEKFRPFYLSQ 292
DB 217 ---NRPSLAELPQAGPETPGLEGKELMQLCWSSEPKRPSFOECLPTDEVFQ-----M 268
OY 293 LEESVEEDVKSLLKKEYSNENAVYKRMQSLQDCVAVPSSRSNSATEQGSLSHSSQGLMG 352
DB 269 VENNMAAIVTYKDFLSQLRSSNRFP-----SIPSS-----GOG 302
OY 353 PVESEWPAFLHPOEENEPISQSLQDEANVHLYGSHMDROTQOPRONAVYNR--ER 411
DB 303 GTEMDFGFRRTIENQSHRNDVYSEWL-----NKLNEEPPSSVPKCPISLTK 349
OY 412 RRRVSHDPFAOQRPVENQNTGKGTVSSAASHGNNAVHOPSGLTSPQVLYONNGLYSS 471
DB 350 KSRAOEEVPOA-----WTAGTSSDSMAQ---PQTPETSTFRNOPS- 389
OY 472 HGFGRPLDPGTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNTPTMPSSSLPPTDESIK- 530
DB 390 -----PISTGT-----PS-----PGRGNOGAEROGMMWSCRTPEPNPVTG 425
OY 531 ---YTIYSTGIQIGAVNYMEIGTSS 554
DB 426 RPLVNIYNCGSGVQVGDNNYLTMOQTTA 452

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RESULT 6

```

; Sequence 231, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273

```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 231
; LENGTH: 518
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-771-161A-231

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Query Match      11.9%; Score 423; DB 10; Length 518;
Best Local Similarity 25.3%; Pred. No. 6.2e-21;
Matches 145; Conservative 95; Mismatches 166; Indels 146; Gaps 22;

```

```

OY 14 SSDPFLSENL-DSGGFGVSLCFHRTGGLMTKTVYKPCNIEHNEALLBEAKMNLRLH 72
DB 17 STELENELVKQKGGFTVFAOHRKMG-----YVAVKIVNSKAIISREVKAMASLDN 69
OY 73 SRVVLGVI-----IEGKYSLYMEYKGNLMHVLKAEKSTPLSVKGRILEIEIGMC 127
DB 70 EFLVRLKEGVIRKVMWDDPKPALVTKFMENGLSGLLQSCPRPWLICRLKKEVVLGMF 129
OY 128 YLHGKG--VIHKDKPENILVNDNFIKIADLGLASFRRMMSKLNNEHNEELREVDTAK- 184
DB 130 YLHDQNPVLLHRDLKPSNVLPDPDLHVKLADFGISTFGGSG-----SGTSGSG 177
OY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVYVIMAFANKE---PYE-----NAICEQ 236
DB 178 EPGGTGLYLAPELVFNVRRASTASDVYSFGILMAYLAEREVELPEPSLYEAVCNRQ 237
OY 237 LIMCIKSNRPDDVDITEYCPRE-----ITSLMKLCWEANPEARPTP---PGIEEKFRP 287
DB 238 -----NRPSLAELPQAGPETPGLEGKELMQLCWSSEPKRPSFOECLPTDEVFQ- 288
OY 288 FYLSQLEESVEEDVKSLLKKEYSNENAVYKRMQSLQDCVAVPSSRSNSATEQGSLSHSSQ 347
DB 289 ---MVENNMAAIVTYKDFLSQLRSSNRFP-----SIPSS----- 320
OY 348 GLGMPVEESWPAFLHPOEENEPISQSLQDEANVHLYGSHMDROTQOPRONAVYNR 407
DB 321 --GGGTEMDFGFRRTIENQSHRNDVYSEWL-----NKLNEEPPSSVPKCPISLTK 365
OY 408 EE-ERRRVSHDPFAOQRPVENQNTGKGTVSSAASHGNNAVHOPSGLTSPQVLYONN 466
DB 366 PSILTKRSRAOEEVPOA-----WTAGTSSDSMAQ---PQTPETSTFRNOPS- 406
OY 467 GLVSSHGFGTRPLDPGTAGPRVWYRPIPSHMPSLHNIIPVETNYLGNTPTMPSSSLPPTD 526
DB 407 QMSK-----PISTGT-----PS-----PGRGNOGAEROGMMWSCRTPEPNPVTG 441
OY 527 ESIR---YTIYSTGIQIGAVNYMEIGTSS 554
DB 442 NPVTGRPLVNIYNCGSGVQVGDNNYLTMOQTTA 473

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RESULT 7

```

; Sequence 2, Application US/10164080
; Publication No. US20030087411A1
; GENERAL INFORMATION:
; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, A.
; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```


Db 74 EMANFRYLPPVYGICQE--PVGLMVEINETSLEKLASE-PLPWDLRRERIVHETAVGGMN 13

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Db      297  DLAHPGEKS-----SLESSEARPESSRLKRASAPPFNDCSLSELLSQL-DSGISO 348

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OY 362 SLEHPOENEPISLOSKL-QDEANVHLVG-SRMDROTKQOPRONVAYNRE 408
 Db 349 TLEGPBELSRSSSECKLIPSSSSGKRLSGVSSVDSAFSSRGLSLISFEFE 397

RESULT 10

US-09-866-050A-409
 ; Sequence 409, Application US/09866050A
 ; Publication No. US20030040471A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Orrust, Rene
 ; APPLICANT: Murison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; FILE REFERENCE: 11000.1011c4U
 ; CURRENT APPLICATION NUMBER: US/09/866,050A
 ; CURRENT FILING DATE: 2001-05-24
 ; NUMBER OF SEQ ID NOS: 725
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 409
 ; LENGTH: 590
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-866-050A-409

Query Match 11.5%; Score 408.5; DB 9; Length 590;
 Best Local Similarity 30.8%; Pred. No. 7.3e-20;
 Matches 126; Conservative 74; Mismatches 164; Indels 45; Gaps 16;

OY 14 SSDPLESABLDGGGFGKVSILCFHRTQGLMIMKT---VYKGPC-IEHNE--ALLEEAKM 67
 Db 20 ACEFAGMEKVGSGGFGQVYKVRH-----VHKWTWIAIKSPSLNHDREMRMLEEAKM 74
 OY 68 NLRHSRYVKLLGVIIEEKYSLVMEYMKGLMHLVAKEMSTPLSVKGRILLETIEGNC 127
 Db 75 ENAKFRYILPVYGIOE--PVLVMEYMETGSLKLEKLASE-PLPMDLFRRIYHETAYGWN 131
 OY 128 YLH--GKGVYHNDLKPENILVNDPHIKIADGLASFWMKSKLNNEHNEHLEVDGTA 185
 Db 132 FLHCHSPPLHLHDLKPAHLIDAHVAKISDGLA-----KCNMSSHDLISMDGLF-- 183
 OY 186 NGCTIYAPAEHLNDVNAKPKTEKSPVYSFAVVLMAIFANKPEYEALICEQOLIMCISGN 245
 Db 184 --GTIAYLPPERIKERSLFDTRKHDVYSFAIYIMGVLLQKKRPADEKNILHIMMKVYAGH 241
 OY 246 RPDVDDITEYCPR---EIIISLMKLCWEANPEARPTFPGIEKFRFYISQLEESYEEDVK 302
 Db 242 RPELPICRPRPRACASLIGIMQRCWADPOVPRPTFOITSE----TEDLCEKPEDEVK 296
 OY 303 SLKREYSNENAVYKRMQSLQDCVAVP--SSRSNSATQPGSLHSSQGLMGVPVESWAP 361
 Db 297 DLAEHPGKES-----SLESKSEARPESSRLKRAAPRPNDGSLSLLEQL--DSGISQ 348
 OY 362 SLEHPOENEPISLOSKL-QDEANVHLVG-SRMDROTKQOPRONVAYNRE 408
 Db 349 TLEGPBELSRSSSECKLIPSSSSGKRLSGVSSVDSAFSSRGLSLISFEFE 397

RESULT 11

US-10-287-594-7
 ; Sequence 7, Application US/10287594
 ; Publication No. US20030096288A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jia
 ; APPLICANT: Dixit, Vishva M
 ; TITLE OF INVENTION: PAID, A NO. US20030096288A1 Death Adaptor Molecule
 ; FILE REFERENCE: 1488.0860002
 ; CURRENT APPLICATION NUMBER: US/10/287,594
 ; CURRENT FILING DATE: 2002-11-05

; PRIOR APPLICATION NUMBER: US/09/545,605
 ; PRIOR FILING DATE: 2001-04-07
 ; PRIOR APPLICATION NUMBER: 08/995,159
 ; PRIOR FILING DATE: 1997-12-19
 ; PRIOR APPLICATION NUMBER: 60,033,868
 ; PRIOR FILING DATE: 1996-12-20
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 77
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-287-594-7

Query Match 11.5%; Score 406; DB 9; Length 77;
 Best Local Similarity 100.0%; Pred. No. 7.1e-21;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 590 IRENIGKHKNCARLGFQSOIDEIDHDYERDGLKEKYOMLOKWMREGIKATYGL 649
 Db 1 IRENIGKHKNCARLGFQSOIDEIDHDYERDGLKEKYOMLOKWMREGIKATYGL 60
 OY 650 AQLHQCRIIDLSSLI 666
 Db 61 AQLHQCRIIDLSSLI 77

RESULT 12

US-09-866-050A-512
 ; Sequence 512, Application US/09866050A
 ; Publication No. US20030040471A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Orrust, Rene
 ; APPLICANT: Murison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; FILE REFERENCE: 11000.1011c4U
 ; CURRENT APPLICATION NUMBER: US/09/866,050A
 ; CURRENT FILING DATE: 2001-05-24
 ; NUMBER OF SEQ ID NOS: 725
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 512
 ; LENGTH: 478
 ; TYPE: PRT
 ; ORGANISM: Rat
 ; US-09-866-050A-512

Query Match 11.4%; Score 405.5; DB 9; Length 478;
 Best Local Similarity 25.5%; Pred. No. 8.8e-20;
 Matches 154; Conservative 80; Mismatches 179; Indels 191; Gaps 28;

OY 10 IKKMSDFLES-AELDSGFGKVSILCFHRTQGLMIMKTGVKPGNCTEHNELLEEAKMN 68
 Db 14 ISLVGSELENLGVGCGGAVFRARHTAMNDVAK-----IYNSKKISREKAVY 66
 OY 69 RLRSRYVKLLGVITE-EGKY---SLVMEYMKGLMHLVAKEMSTPLSVKGRILLETI 123
 Db 67 NLRHENVLLLGVTENEMDYVYGPALVTFGMENGLSLGLQSPCRPWLICRLLEEV 126
 OY 124 EGMCTYLH--GKGVYHNDLKPENILVNDPHIKIADGLASFWMKSKLNNEHNEHLEVDG 181
 Db 127 LGMCTYLSLNPSLIHRDLKPSNVLLDELAKLADGSLTFQGSOGS-----GS 177
 OY 182 TARKNGSTIYAPAEHLNDVNAKPKTEKSPVYSFAVVLMAIFANKPE-----YENATC 233
 Db 178 GSRDSGGLTAYLAPE-LTDMDKASKASDVYSGVLTWYVLAGREAYVDKSLIRGAVC 236
 OY 234 EQLIMCISGNRPDVDDITEYCPRE-----IISLMKLCWEANPEARPTFPGIEKFRFP 288

Db 237 NRO-----RRPPLTEPPDSEPTPEGLKELMTWCHMSSEPKDRPSFODESKTNNV 288
 QY 289 YLSQLESVEEDYKSLK---KEYSNENAVYKRMOSLO---LDCVAVPSSRSMSATPOPG 341
 Db 289 YI-LVDDKDAASVKVHYLSQYRSSDTKLASARESSOKGTEVDC---PRETIYEMLD 342
 QY 342 SLHSSQGLGKMGVPEESWFAFSLHEPOEENEPISQSLQDEANLYGSRMDROTQKQOPRQ 401
 Db 343 RLH-----LEEPS-----GSVERLISL-----360
 QY 402 NVAYNBEERRRRVSHDPFAQOPRYENFONTEGKGTIVYSSAASHGNAVHOPSGILTSO--- 458
 Db 361 -----TERRG-----KEASFGHAT---PAGTSQDTLA 384
 QY 459 --POVLXONGLXSSHGFGTRPLDPTGACRVRVYRPIPSHPSLHNPVETN----- 509
 Db 385 GTPQIPIH---TLPSKGTTPRPAPFTETPGD-----PQRQOGGRNS 422
 QY 510 ---YLGNTPMPFSSLPPTDESIRKTYINSTGIGIAGAVNYMEIGTSSSLDSTNNTF-K 565
 Db 423 NPMYTNMARN-PMTGL-----QST--VLNCSFVOIGOHNCMSV-----QPRTAFPK 466
 QY 566 EEPFA 569
 Db 467 KEPA 470

RESULT 13
 US-10-112-793-27
 ; Sequence 27, Application US/10112793
 ; Publication No. US20020192729A1
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/112.793
 FILING DATE: 28-Mar-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/828.683A
 FILING DATE: 31-Mar-1997
 APPLICATION NUMBER: 08/625328
 FILING DATE: 1-Apr-1996
 APPLICATION NUMBER: 08/710802
 FILING DATE: 23-Sep-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Marschang, Diane L.
 REGISTRATION NUMBER: 35,600
 REFERENCE/DOCKET NUMBER: P1007P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/223-5416
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 77 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-10-112-793-27

Query Match 11.3%; Score 402; DB 9; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.3e-20;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 590 IRENLGKMMKNCARKLGFTQSQIDEIDHDYERDGLKEKYVQMLQKVMREGIGATVQKL 649
 Db 1 IRENLGKMMKNCARKLGFTQSQIDEIDHDYERDGLKEKYVQMLQKVMREGIGATVQKL 60
 QY 650 AQALHQCSTRIDLSL 665
 Db 61 AQALHQCSTRIDLSL 76

RESULT 14
 US-10-164-080-7
 ; Sequence 7, Application US/10164080
 ; Publication No. US20030087411A1
 ; GENERAL INFORMATION:
 APPLICANT: BIRD, Timothy, A.
 APPLICANT: HOLLAND, Pamela, M.
 APPLICANT: PESCHON, Jacques, J.
 TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND
 FILE REFERENCE: 3280-B
 CURRENT APPLICATION NUMBER: US/10/164,080
 CURRENT FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: 60/295,959
 PRIOR FILING DATE: 2001-06-04
 PRIOR APPLICATION NUMBER: 60/334,362
 PRIOR FILING DATE: 2001-11-29
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 7
 LENGTH: 784
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-164-080-7

Query Match 10.8%; Score 384; DB 9; Length 784;
 Best Local Similarity 30.1%; Pred. No. 5e-18;
 Matches 120; Conservative 73; Mismatches 146; Indels 60; Gaps 17;

QY 14 SSDFLESALDSSGFGKYSICFHRTOGLMTKT---YKPPNC-IEHNE--ALLEPKMM 67
 Db 19 AGEFTGMEKVGSGGFGQVYKVRH---VHMKTWLAIKSPSLHVDREMEELLEBAKKM 73
 QY 68 NRLRHSRVKLLGVIIIEGKYSIVMEYMEKGNLMHYLKAKMSPLSVKGRILEIEIGMC 127
 Db 74 EAKFRYILPVYIGCRE--PVGLVMEYMETGSLLEKLASE-PLPMDIRFRIIETAVGMN 130
 QY 128 YLH--GKGYIHDKLEPNILVNDPFIKTLADLGLASFKMSKLNNEHNELEREVDGTAKK 185
 Db 131 FLHGMAPRLHLHLKPRANILLDAHNYHKISDFGLA-----KONGLSHSDLDMDGLF-- 182
 QY 186 NGCTLYYMAPEHLNDVNAKTEKSDVYSPAVYVMAIFANKPEPENAICEQOLIMCKSKN 245
 Db 183 --GTIAVLPPEIRERKRSLEDTKHDVYSFAIVMGVLTQKPPADEKNILHIWVKVKGH 240
 QY 246 RPVVDITEXCPR---EISIMKLCWMEANFEARPTPGIEKRRPFLYSOLEESVEE--- 299
 Db 241 RPLPVPYCARPRACSHLILMORWOGDPRVPRPTFOELTSETEDL-CEKPDDEVAKETAH 299
 QY 300 --DVKSS-----LKK-----EYSNENAVYKRMOSLOD-----CVAVPS--SRSN 334
 Db 300 DLDPVKSPPERSRVVAPRLKRAASAPTFENDNYSLELLS--QLDSGVSAVEGPEELSRSS 357
 QY 335 SATEQPSGLHSSQGLGKMGVPEESWFAFSLHEPOEENEPS 373
 Db 358 SESKLPSSGSKRLSGVSSVDASFASSGSLSLSFEREPS 396

RESULT 15

Query Match	10.6%	Score 375.5;	DB 9;	Length 536;
Best Local Similarity	29.8%;	Pred. No. 1.1e-17;		
Matches 122; Conservative	71;	Mismatches 172;	Indels 45;	Gaps 16

[illegible]

Search completed: June 21, 2003, 16:22:18
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2003, 15:50:12 : Search time 73 Seconds
(without alignments)
1224.810 Million cell updates/sec

Title: US-09-981-397a-16
Perfect score: 3545
Sequence: 1 MOPDMSLVNVIKMKSDPLES.....ALHQCSRIDLSSLIYVSON 671

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3545	100.0	671	21	AAV78502
2	3545	100.0	671	22	ABG16302
3	3545	100.0	671	22	ABG16302
4	3545	100.0	671	23	ABAB2091
5	3545	100.0	671	23	ABAB3794
6	3539	99.8	671	23	AAU80370
7	3513	99.1	671	18	AAV15461
8	2423.5	68.4	656	18	AAW04627
9	2416.5	68.2	656	20	AAW80994
10	1529	43.1	948	22	ABG16304

11	433	12.2	518	21	AAAB01524	Kinase of death (K
12	433	12.2	518	22	AAAB01526	Kinase of death (K
13	433	12.2	518	21	AAE09430	Human kinase of de
14	433	12.2	518	22	AAE09432	Human kinase of de
15	432	12.2	518	21	AAE09430	Kinase of death (K
16	432	12.2	518	22	AAE09436	Human kinase of de
17	428.5	12.1	555	22	AAE07392	Novel central nerv
18	428	12.1	497	22	AAE66604	Human h15590 prote
19	425	12.0	518	21	AAAB01525	Kinase of death (K
20	425	12.0	518	22	AAE09431	Human kinase of de
21	423	11.9	427	22	AAW93664	Human polypeptide
22	423	11.9	519	21	AAV45042	Human Apop3 protei
23	423	11.9	519	21	AAV45046	Human Apop3 (K50P)
24	414	11.7	420	21	AAAB01529	Kinase of death (K
25	414	11.7	420	22	AAE09435	Human kinase of de
26	413.5	11.7	485	21	AAE18658	A human regulator
27	410.5	11.6	786	21	AAE69163	Amino acid sequenc
28	410.5	11.6	787	21	AAV76079	Murine protein kin
29	410.5	11.6	787	22	AAE56018	Skin cell protein,
30	410.5	11.6	787	23	ABE72218	Murine protein iso
31	408.5	11.5	590	21	AAV76123	Murine RIP protein
32	408.5	11.5	590	22	AAE56062	Skin cell protein,
33	408.5	11.5	590	23	ABE72262	Murine protein iso
34	408.5	11.5	763	21	AAV79154	Mouse protein kina
35	405.5	11.4	478	22	AAE20345	Rat RIP-3-like dea
36	405.5	11.4	478	23	ABE72298	Rat protein isolat
37	401.5	11.3	436	21	AAV45043	Human Apop3 (1-436
38	388.5	11.0	261	21	AAE01527	Kinase of death (K
39	388.5	11.0	261	22	AAE09433	Human kinase of de
40	387	10.9	784	22	AAE94037	Human protein sequ
41	384	10.8	784	23	AAE53291	Human polypeptide
42	377.5	10.6	437	21	AAV45047	Human Apop3 (82-51
43	375.5	10.6	536	21	AAV76007	Murine RIP protein
44	375.5	10.6	536	22	AAE55946	Skin cell protein,
45	375.5	10.6	536	23	ABE72146	Murine protein iso

ALIGNMENTS

RESULT 1	
AAV78502	standard; Protein: 671 AA.
ID	AAV78502
XX	
AC	AAV78502;
XX	
DT	05-MAY-2000 (first entry)
XX	
DE	Human RIP-1 amino acid sequence.
XX	
KW	RIP-1; RaBP; RLIP; antisense inhibitor; anti-inflammatory; cytostatic; anti-infective; diagnose; prevent; treatment; tumour formation.
XX	
OS	Homo sapiens.
XX	
PN	US6020198-A.
XX	
PD	01-FEB-2000.
XX	
PF	25-SEP-1998; 98US-0161443.
XX	
PR	25-SEP-1998; 98US-0161443.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
PI	Bennett CF, Cowser LM;
XX	
DR	WPI: 2000-146889/13.
DR	N-PSDB; AAZ89748.
XX	
FT	Antisense inhibition of human RIP-1 expression, useful for diagnosing,
PT	preventing and treating conditions such as inflammation -
XX	

PS Disclosure: Column 29-36; 26pp; English.

XX This sequence represents the human RIP-1 amino acid sequence. RIP-1 (also
CC known as Ralpl1 and R1P) is a GTPase activating protein (GAP) thought to
CC be a downstream target of Ral. The invention relates to RIP-1 antisense
CC phosphorothioate oligonucleotides with anti-infective, anti-inflammatory
CC and cytostatic activity. The oligonucleotides are RIP-1 antisense
CC inhibitors and are used in the diagnosis, prevention and treatment of
CC conditions associated with RIP-1 expression. Conditions associated with
CC RIP-1 expression include various infections, inflammation and tumour
CC formation.

XX Sequence 671 AA;

Query Match 100.0%; Score 3545; DB 21; Length 671;
Best Local Similarity 100.0%; Pred. No. 6,4e-281;

Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MOPDMSLVNTIKMSSDFLESADLDSGFGKVSICFHRTOGLMIMTKVYKGPCNIEHNEAL 60
DB 1 MOPDMSLVNTIKMSSDFLESADLDSGFGKVSICFHRTOGLMIMTKVYKGPCNIEHNEAL 60
QY 61 LEEAKMMNRLRHSRVKLLGVIIIEEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
DB 61 LEEAKMMNRLRHSRVKLLGVIIIEEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
QY 121 EIIIEGMCYLHGKGVIIHKDLKPNILVNDNFHRIADLGLASFPMWSKLNNEHNEALREV 180
DB 121 EIIIEGMCYLHGKGVIIHKDLKPNILVNDNFHRIADLGLASFPMWSKLNNEHNEALREV 180
QY 181 GTAKKNGGTLTYMAPHLDVNAKPTKESDVYSFAVVLMAIFANKEPYENALICEQOLIMC 240
DB 181 GTAKKNGGTLTYMAPHLDVNAKPTKESDVYSFAVVLMAIFANKEPYENALICEQOLIMC 240
QY 241 IKSNGRPDVTITEYCPREIISLMKLCWANEAPRTPEIGIEKRPFLTSQLESVEED 300
DB 241 IKSNGRPDVTITEYCPREIISLMKLCWANEAPRTPEIGIEKRPFLTSQLESVEED 300
QY 301 VSLIKKEYSNENAVYKRMOSLOLDCVAVPSRSNSATEQPGSLHSSOGIGMGVPEESMFA 360
DB 301 VSLIKKEYSNENAVYKRMOSLOLDCVAVPSRSNSATEQPGSLHSSOGIGMGVPEESMFA 360
QY 361 PSLHEPHEENEPISLOSKLODEANHYHLYGSRMDROTQOPROWAVANREERERRRVSHPDF 420
DB 361 PSLHEPHEENEPISLOSKLODEANHYHLYGSRMDROTQOPROWAVANREERERRRVSHPDF 420
QY 421 AOOQREYENFONTEGKGVYSSAASHGNVHOPSGILTPOVLYONNGLYSSHGCTRPDL 480
DB 421 AOOQREYENFONTEGKGVYSSAASHGNVHOPSGILTPOVLYONNGLYSSHGCTRPDL 480
QY 481 PGTAGPRVWYRPIPSHMPSLNHIPTPEYNYLGNPTMPFSSLPPTDESIRKTYIYNSTGIIQ 540
DB 481 PGTAGPRVWYRPIPSHMPSLNHIPTPEYNYLGNPTMPFSSLPPTDESIRKTYIYNSTGIIQ 540
QY 541 IGAIVNYMEIGTSSSLDSTNTNFKKEPAKYQALFNDTTLSTLKHDPITENIGKHAKN 600
DB 541 IGAIVNYMEIGTSSSLDSTNTNFKKEPAKYQALFNDTTLSTLKHDPITENIGKHAKN 600
QY 601 CARLKGTFQSOIDELIDHDYERDGLKEKYOMLOKVMWMEGICATGVLQAOLHQCRRID 660
DB 601 CARLKGTFQSOIDELIDHDYERDGLKEKYOMLOKVMWMEGICATGVLQAOLHQCRRID 660
QY 661 LLSSTLIYSON 671
DB 661 LLSSTLIYSON 671

```

RESULT 2

ABG16302
ID ABG16302 standard; Protein: 671 AA.
XX ABG16302;
XX

DT 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #16293.

DE Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HUSE-) HSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB: AAS80489.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 46661; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.

XX Sequence 671 AA;

Query Match 100.0%; Score 3545; DB 22; Length 671;
Best Local Similarity 100.0%; Pred. No. 6,4e-281;

Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MOPDMSLVNTIKMSSDFLESADLDSGFGKVSICFHRTOGLMIMTKVYKGPCNIEHNEAL 60
DB 1 MOPDMSLVNTIKMSSDFLESADLDSGFGKVSICFHRTOGLMIMTKVYKGPCNIEHNEAL 60
QY 61 LEEAKMMNRLRHSRVKLLGVIIIEEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
DB 61 LEEAKMMNRLRHSRVKLLGVIIIEEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
QY 121 EIIIEGMCYLHGKGVIIHKDLKPNILVNDNFHRIADLGLASFPMWSKLNNEHNEALREV 180
DB 121 EIIIEGMCYLHGKGVIIHKDLKPNILVNDNFHRIADLGLASFPMWSKLNNEHNEALREV 180
QY 181 GTAKKNGGTLTYMAPHLDVNAKPTKESDVYSFAVVLMAIFANKEPYENALICEQOLIMC 240

```

```

Db      181  GTAKNGTLYYMAPEHLNDVNAKPTKSDVYFAVWLMAIFANKPEYENAIICEQLIMC 240
Qy      241  IKSNRPDVDDITCYCREITISLMKLCMEANPEARPTPGIEEFPRTYSOLESEVED 300
Db      241  IKSNRPDVDDITCYCREITISLMKLCMEANPEARPTPGIEEFPRTYSOLESEVED 300
Qy      301  VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 360
Db      301  VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 360
Qy      361  PSLEHPOEENEPISQSLQDEANYHLVGSMDROTQKOPRONVAVNREERRRRVSHDPF 420
Db      361  PSLEHPOEENEPISQSLQDEANYHLVGSMDROTQKOPRONVAVNREERRRRVSHDPF 420
Qy      421  AQORPYNFONTEKGTVYSSAASHGNAVHQPGLTSQPOVLYONNGLYSHGFGTRPLD 480
Db      421  AQORPYNFONTEKGTVYSSAASHGNAVHQPGLTSQPOVLYONNGLYSHGFGTRPLD 480
Qy      481  PGTAGPVRWYRPIPSHNPSLHNIIVPTNYLGNTPTMPFSSLPTDESIKTYINSTGIC 540
Db      481  PGTAGPVRWYRPIPSHNPSLHNIIVPTNYLGNTPTMPFSSLPTDESIKTYINSTGIC 540
Qy      541  IGAVNMEIGTSSSLDSTNTNFKKEPPAKYQAI FDNPTSLTDKHLDPIRENLGKHWKN 600
Db      541  IGAVNMEIGTSSSLDSTNTNFKKEPPAKYQAI FDNPTSLTDKHLDPIRENLGKHWKN 600
Qy      601  CARLGTQSOIDIDHDYERDGLKERYOMLOKWVAREGKGYVKKLAQALHQCSDID 660
Db      601  CARLGTQSOIDIDHDYERDGLKERYOMLOKWVAREGKGYVKKLAQALHQCSDID 660
Qy      661  LLSLIYVSON 671
Db      661  LLSLIYVSON 671

```

RESULT 3
AAB82091
ID AAB82091 standard; Protein: 671 AA.

```

XX      XX      AAB82091:
XX      XX      28-JUN-2001 (first entry)
XX      XX      Human Receptor Interacting Protein, hrpP.
DE      DE      Human Receptor Interacting Protein, hrpP.
KW      KW      Human Receptor Interacting Protein; hrpP; antibacterial; cytostatic;
KW      KW      antiinflammatory; gene therapy; infection; genetic disease; neoplasia;
KW      KW      Tumour necrosis factor Receptor Associated Factor-2; TRAF2; TRAFD;
KW      KW      Tumour necrosis factor Receptor Associated Death Domain protein;
XX      XX      inflammation; hypersensitivity.
OS      OS      Homo sapiens.
XX      XX
FH      FH      Key
FT      FT      Domain
FT      FT      Location/Qualifiers
FT      FT      1..300
FT      FT      /label= Kinase_domain
FT      FT      509..518
FT      FT      /label= alpha-delta1
FT      FT      /note= "Specifically claimed in Claim 6"
FT      FT      514..521
FT      FT      /label= alpha-delta2
FT      FT      /note= "Specifically claimed in Claim 7"
FT      FT      506..514
FT      FT      /label= alpha-delta3
FT      FT      /note= "Specifically claimed in Claim 8"
FT      FT      504..524
FT      FT      /label= alpha-delta4
FT      FT      /note= "Specifically claimed in Claim 9"
FT      FT      498..514
FT      FT      /label= alpha-delta5
FT      FT      /note= "Specifically claimed in Claim 10"
FT      FT      514..534
FT      FT      Region

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FT      FT      /label= alpha-delta6
FT      FT      /note= "Specifically claimed in Claim 11"
FT      FT      513..520
FT      FT      /label= alpha-delta7
FT      FT      /note= "Specifically claimed in Claim 12"
FT      FT      508..515
FT      FT      /label= alpha-delta8
FT      FT      /note= "Specifically claimed in Claim 13"
FT      FT      512..522
FT      FT      /label= alpha-delta9
FT      FT      /note= "Specifically claimed in Claim 14"
FT      FT      423..514
FT      FT      /label= alpha-delta10
FT      FT      /note= "Specifically claimed in Claim 15"
FT      FT      423..543
FT      FT      /label= alpha-delta11
FT      FT      /note= "Specifically claimed in Claim 16"
FT      FT      423..579
FT      FT      /label= alpha-delta12
FT      FT      /note= "Specifically claimed in Claim 17"
FT      FT      423..633
FT      FT      /label= alpha-delta13
FT      FT      /note= "Specifically claimed in Claim 18"
FT      FT      423..671
FT      FT      /label= alpha-delta14
FT      FT      /note= "Specifically claimed in Claim 19"
FT      FT      514..543
FT      FT      /label= alpha-delta15
FT      FT      /note= "Specifically claimed in Claim 20"
FT      FT      514..579
FT      FT      /label= alpha-delta16
FT      FT      /note= "Specifically claimed in Claim 21"
FT      FT      514..633
FT      FT      /label= alpha-delta17
FT      FT      /note= "Specifically claimed in Claim 22"
FT      FT      514..671
FT      FT      /label= alpha-delta18
FT      FT      /note= "Specifically claimed in Claim 23"

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XX      XX      US6211337-B1
XX      XX      03-APR-2001
XX      XX      11-AUG-1998; 98US-0132118.
XX      XX      23-OCT-1995; 95US-0553727.
XX      XX      (TULA-) TULARIK INC.
XX      XX      Baichwal VR, Huang J, Hsu H, Goeddel DV;
XX      XX      WPI: 2001-334617/35;
XX      XX      N-PSDB: AAF86480.
XX      XX      New receptor interacting protein polypeptide having threonine in
XX      XX      position 514 useful in screening assays for agents that modulate
XX      XX      interaction of protein with its binding targets
XX      XX      Claim 24: Columns 13-16; 10pp; English.

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The present sequence is human Receptor Interacting Protein (RIP). RIP is useful in screening assays for agents that modulate the interaction of RIP with its natural binding targets, especially substrates such as Tumour necrosis factor Receptor Associated Factor-2 (TRAF2) and Tumour necrosis factor Receptor Associated Death Domain protein (TRADD). The agents are potentially useful for the treatment and diagnosis of diseases, e.g. infections, genetic diseases, neoplasia, inflammation and hypersensitivity.

Sequence 671 AA;
Query Match 100.0%; Score 3545; DB 22; Length 671;
Best local Similarity 100.0%; Pred. No. 6,4e-281;

	Matches	671: Conservative	0: Mismatches	0: Indels	0: Gaps	0:
QY	1	MQPMDSLNVIKMKSSDFLESALDSDGGFGKVSICFHRTQGLIMKTYKGCNCEIHNHAL	60			
Db	1	MQPMDSLNVIKMKSSDFLESALDSDGGFGKVSICFHRTQGLIMKTYKGCNCEIHNHAL	60			
QY	61	LEAKAMNRLHRSRVKLLGVIIIEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL	120			
Db	61	LEAKAMNRLHRSRVKLLGVIIIEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL	120			
QY	121	ETIEGMCYLGKGVYIHKDKPENILVNDPFHKTADGLASFCKMSKLNNEHNELREVD	180			
Db	121	ETIEGMCYLGKGVYIHKDKPENILVNDPFHKTADGLASFCKMSKLNNEHNELREVD	180			
QY	181	GTAKNGGTLYYMAPEHLNDVNAKPTKSDVYSEAVVLMALFANKPEYENALICEQOLIMC	240			
Db	181	GTAKNGGTLYYMAPEHLNDVNAKPTKSDVYSEAVVLMALFANKPEYENALICEQOLIMC	240			
QY	241	IKSGNRPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSQLEESVEED	300			
Db	241	IKSGNRPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSQLEESVEED	300			
QY	301	VKSLLKKESENNAVYKRMQSLQDLCVAVPSSRSNSATQPSGLSHSSOGLGMPVEESWFA	360			
Db	301	VKSLLKKESENNAVYKRMQSLQDLCVAVPSSRSNSATQPSGLSHSSOGLGMPVEESWFA	360			
QY	361	PSLEHPOENEPSSLOSKLODEANHYLGSRRDROTKOOPRONVAYNREERRRVSHDPF	420			
Db	361	PSLEHPOENEPSSLOSKLODEANHYLGSRRDROTKOOPRONVAYNREERRRVSHDPF	420			
QY	421	AQORPYENFQNTGEGKTVYSSAASHGNVHQPSCGLTSOPVLYONNGLYSSHGFGTRPLD	480			
Db	421	AQORPYENFQNTGEGKTVYSSAASHGNVHQPSCGLTSOPVLYONNGLYSSHGFGTRPLD	480			
QY	481	PGTGPRVYVPIPSHMPSLNIPPTETNYLGNTPTMFPSSLPDESIKTYIYNSTGIQ	540			
Db	481	PGTGPRVYVPIPSHMPSLNIPPTETNYLGNTPTMFPSSLPDESIKTYIYNSTGIQ	540			
QY	541	IGAVNYMEIGTSSSLDSTNTNFKKEPAKYQAFDMTSTSLTDKHLPIRENIGKMHKN	600			
Db	541	IGAVNYMEIGTSSSLDSTNTNFKKEPAKYQAFDMTSTSLTDKHLPIRENIGKMHKN	600			
QY	601	CARKIGTQSOIDELDHDIYERDGLKEKYOMLQKVMREGIKGATVGLAQLHQCRRID	660			
Db	601	CARKIGTQSOIDELDHDIYERDGLKEKYOMLQKVMREGIKGATVGLAQLHQCRRID	660			
QY	661	LLSSLIYSON 671				
Db	661	LLSSLIYSON 671				

RESULT 4
ABB83794
ID ABB83794 standard; Protein: 671 AA.

03-SEP-2002 (first entry)

Human RIP.
Human; RIP; cell death protein RIP; receptor interacting protein; serine/threonine protein kinase; enzyme; immunosuppressive; cardiact; cerebroprotective; neuroprotective; antiparkinsonian; virucide; antirheumatic; antidiabetic; dermatological; death receptor; caspase; necrosis; immune system; autoimmune disease; multiple sclerosis; diabetes; rheumatoid arthritis; infection; neurological disease; Alzheimer's disease; Parkinson's disease; viral; signal transduction.

Homo sapiens.
XX OS
XX PN
WO2000236148-A2.

XX	10-MAY-2002.
PD	Best Local Similarity 100.0%; Score 3545; DB 23; Length 671;
XX	26-OCT-2001; 2001WO-EP12440.
PR	02-NOV-2000; 2000DE-1054279.
XX	(Apot-) APOTECH RES & DEV LTD.
PI	Tschopp J, Holler N;
XX	WPI: 2002-519224/55.
DR	N-PSDB: ABN81397.
XX	Use of a death receptor ligand or receptor interacting protein to induce necrotic cell death, useful for treating e.g. autoimmune disease, also their inhibitors.
PS	Disclosure: Fig 7; 56pp; German.
XX	The invention relates to the use of a ligand (I) of the death receptor or its functional derivative, for inducing caspase-independent (i.e. necrotic) death (CID) in cells, especially those of the immune system. (I) are used to induce CID of peripheral blood lymphocytes, especially activated T cell for treatment of autoimmune diseases. Also CID can be inhibited by using agents (II) that bind to (I), or agents (III) that inhibit function of RIP (receptor-interacting protein), particularly for treatment of autoimmune diseases (e.g. multiple sclerosis, diabetes, lupus or rheumatoid arthritis); cardiac infarction; cerebral stroke; or neurological diseases (Alzheimer's or Parkinson's). (III) can also be used to treat diseases associated, at least in part, with pathological hypernecrosis and viral infections. The ligand modulates signal transduction through RIP or the death receptor. The present sequence is that of the human cell death protein RIP, a serine/threonine kinase, of the invention.
CC	Sequence 671 AA;
CC	Query Match 100.0%; Score 3545; DB 23; Length 671;
CC	Best Local Similarity 100.0%; Pred. No. 6.4e-281;
CC	Matches 671: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MQPMDSLNVIKMKSSDFLESALDSDGGFGKVSICFHRTQGLIMKTYKGCNCEIHNHAL 60
Db	1 MQPMDSLNVIKMKSSDFLESALDSDGGFGKVSICFHRTQGLIMKTYKGCNCEIHNHAL 60
QY	61 LEAKAMNRLHRSRVKLLGVIIIEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
Db	61 LEAKAMNRLHRSRVKLLGVIIIEGKYSLVMEYMEKGNLMHVLAEMSTPLSVKGRITL 120
QY	121 ETIEGMCYLGKGVYIHKDKPENILVNDPFHKTADGLASFCKMSKLNNEHNELREVD 180
Db	121 ETIEGMCYLGKGVYIHKDKPENILVNDPFHKTADGLASFCKMSKLNNEHNELREVD 180
QY	181 GTAKNGGTLYYMAPEHLNDVNAKPTKSDVYSEAVVLMALFANKPEYENALICEQOLIMC 240
Db	181 GTAKNGGTLYYMAPEHLNDVNAKPTKSDVYSEAVVLMALFANKPEYENALICEQOLIMC 240
QY	241 IKSGNRPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSQLEESVEED 300
Db	241 IKSGNRPDVDDITEYCPREIISLMKLCWEANPEARPTPGIEEKRFPYLSQLEESVEED 300
QY	301 VKSLLKKESENNAVYKRMQSLQDLCVAVPSSRSNSATQPSGLSHSSOGLGMPVEESWFA 360
Db	301 VKSLLKKESENNAVYKRMQSLQDLCVAVPSSRSNSATQPSGLSHSSOGLGMPVEESWFA 360
QY	361 PSLEHPOENEPSSLOSKLODEANHYLGSRRDROTKOOPRONVAYNREERRRVSHDPF 420
Db	361 PSLEHPOENEPSSLOSKLODEANHYLGSRRDROTKOOPRONVAYNREERRRVSHDPF 420
QY	421 AQORPYENFQNTGEGKTVYSSAASHGNVHQPSCGLTSOPVLYONNGLYSSHGFGTRPLD 480
Db	421 AQORPYENFQNTGEGKTVYSSAASHGNVHQPSCGLTSOPVLYONNGLYSSHGFGTRPLD 480

QY 481 PGTAGPRWYRPIPSHMPSLHNPVETNYLGTPTMPFSSLPPTDESIRKTYTYNSTGIG 540
 DB 481 PGTAGPRWYRPIPSHMPSLHNPVETNYLGTPTMPFSSLPPTDESIRKTYTYNSTGIG 540
 QY 541 IGAYNMEIGTSSSLDSTNTNFKKEPPAKYOAIEDNTTSLTDKHLDPRENLGKHWKN 600
 DB 541 IGAYNMEIGTSSSLDSTNTNFKKEPPAKYOAIEDNTTSLTDKHLDPRENLGKHWKN 600
 QY 601 CARKLGFTOSQIDEIDHDYERDGLKEKYVOMLOKWMVREGIKGATVGLQAOLHOCSTRID 660
 DB 601 CARKLGFTOSQIDEIDHDYERDGLKEKYVOMLOKWMVREGIKGATVGLQAOLHOCSTRID 660
 QY 661 LLSLLIYVSON 671
 DB 661 LLSLLIYVSON 671

RESULT 5
 AAU80370
 ID AAU80370 standard; Protein; 671 AA.
 XX
 AC AAU80370;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Human cellular kinase RIP protein.
 XX
 DE Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;
 KM RIP; NCK-interacting kinase; MKK3; SRPK-2.
 KW
 XX Homo sapiens.
 OS
 XX
 PN EP1201765-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 15-OCT-2001; 2001EP-0124604.
 XX
 PR 16-OCT-2000; 2000US-240750P.
 XX
 PA (AXXI-) AXXIMA PHARM AG.
 XX
 PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
 DR MPI: 2002-373930/41.
 DR N-PSDB; ABK51170.
 XX
 PT Identifying agents for treatment or prevention of cytomegalovirus
 PT infection, comprises contacting test compound with cellular kinase and
 PT detecting change in cellular kinase activity -
 XX
 PS Disclosure; Page 27-28; 49pp; English.
 XX
 CC The present invention relates to a new method for identifying compounds
 CC for treating and/or preventing cytomegalovirus (CMV) infection and/or
 CC related diseases. The method of the invention comprises contacting a
 CC test compound with at least one of the cellular kinases RICK, RIP,
 CC NCK-interacting kinase, MKK3 and SRPK-2 and detecting any change in
 CC kinase activity. The method of the invention can be used to treat and/or
 CC prevent CMV infections and related diseases. Oligonucleotides that can
 CC detect the specified kinases can also be used for diagnosis of infection.
 CC The present amino acid sequence represents the human cellular kinase RIP
 CC protein of the invention, as described above.
 CC
 SO Sequence 671 AA:

Query Match 100.0%; Score 3545; DB 23; Length 671;
 Best local similarity 100.0%; Pred. No. 6, 4e-281;
 Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOPDMSLNVIKMKSSDFLESSELDSGGFGKVSICFHRTOGLMIMKTIVYKGPNCIEHNEAL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1 MOPDMSLNVIKMKSSDFLESSELDSGGFGKVSICFHRTOGLMIMKTIVYKGPNCIEHNEAL 60
 QY 61 LEEAKMNNRLRHSRRVYKLLGVITIEEKKYSLVMEYMEKGNLMHLYAKEMSTPLSVKGRIL 120
 DB 61 LEEAKMNNRLRHSRRVYKLLGVITIEEKKYSLVMEYMEKGNLMHLYAKEMSTPLSVKGRIL 120
 QY 121 EIEEGMCLYHGKGVYHKKDLKPNILVNDNFHRIADLGLASFPMWSKLNNEEHNEELREVD 180
 DB 121 EIEEGMCLYHGKGVYHKKDLKPNILVNDNFHRIADLGLASFPMWSKLNNEEHNEELREVD 180
 QY 181 GTAKKNGGTYLYAPPEHLNDVNAKPTKESVYSPFAYVLAIFANKPEYEAATEOOLIMC 240
 DB 181 GTAKKNGGTYLYAPPEHLNDVNAKPTKESVYSPFAYVLAIFANKPEYEAATEOOLIMC 240
 QY 241 IKSGNRPDDVDITEYCPRETIISLMKLCWENPAPRPTFGIEKFRFYLSQLEESVEED 300
 DB 241 IKSGNRPDDVDITEYCPRETIISLMKLCWENPAPRPTFGIEKFRFYLSQLEESVEED 300
 QY 301 VKSLEKEYSNENAVVRMOSLODCVAVPSSRSNSATEOPGSLHSSOGLCMGPVEESWFA 360
 DB 301 VKSLEKEYSNENAVVRMOSLODCVAVPSSRSNSATEOPGSLHSSOGLCMGPVEESWFA 360
 QY 361 PSLFHPQEEENPESLOSXLQDEANYHLGSRMDQOTKOQPRONYAVNBEERRRRVSHDPF 420
 DB 361 PSLFHPQEEENPESLOSXLQDEANYHLGSRMDQOTKOQPRONYAVNBEERRRRVSHDPF 420
 QY 421 AOCRPYENFONTEGKGVYSSASHGNAVHOPSGLTSPQVLYONNGTLYSSHGFGTRPLD 480
 DB 421 AOCRPYENFONTEGKGVYSSASHGNAVHOPSGLTSPQVLYONNGTLYSSHGFGTRPLD 480
 QY 481 PGTAGPRWYRPIPSHMPSLHNPVETNYLGTPTMPFSSLPPTDESIRKTYTYNSTGIG 540
 DB 481 PGTAGPRWYRPIPSHMPSLHNPVETNYLGTPTMPFSSLPPTDESIRKTYTYNSTGIG 540
 QY 541 IGAYNMEIGTSSSLDSTNTNFKKEPPAKYOAIEDNTTSLTDKHLDPRENLGKHWKN 600
 DB 541 IGAYNMEIGTSSSLDSTNTNFKKEPPAKYOAIEDNTTSLTDKHLDPRENLGKHWKN 600
 QY 601 CARKLGFTOSQIDEIDHDYERDGLKEKYVOMLOKWMVREGIKGATVGLQAOLHOCSTRID 660
 DB 601 CARKLGFTOSQIDEIDHDYERDGLKEKYVOMLOKWMVREGIKGATVGLQAOLHOCSTRID 660
 QY 661 LLSLLIYVSON 671
 DB 661 LLSLLIYVSON 671

RESULT 6
 AAM15461
 ID AAM15461 standard; Protein; 671 AA.
 XX
 AC AAM15461;
 XX
 DT 20-JUL-1997 (first entry)
 XX
 DE Human receptor interaction protein.
 XX
 KW Receptor interaction protein; RIP; tumour necrosis factor;
 KW signal transduction; neoplasia; hypersensitivity; inflammation;
 KW diagnosis; therapy.
 XX
 OS Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Domain 1..300
 FT /label= kinase_domain
 XX
 PN WC97J5586-A1.
 XX
 PD 01-MAY-1997.
 XX
 PF 17-OCT-1996; 96WO-US16778.
 XX

Best Local Similarity 99.3%; Pred. No. 2.7e-278;
Matches 666; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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OY 1 MOPDMSLVNIMKSSDLESAELDSGGGKVSICFHRQGLIMKTIVKGPNCIEHNEAL 60
Db 1 MOPDMSLVNIMKSSDLESAELDSGGGKVSICFHRQGLIMKTIVKGPNCIEHNEAL 60
OY 61 LEEAKMNRRLRHSRVKLVGLVIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSYGRITL 120
Db 61 LEEAKMNRRLRHSRVKLVGLVIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSYGRITL 120
OY 121 EIIEGMCLHKGKVIHDKLPENILVNDPFHRIKIDGLASFWMKSKLNNEEHNELREVD 180
Db 121 EIIEGMCLHKGKVIHDKLPENILVNDPFHRIKIDGLASFWMKSKLNNEEHNELREVD 180
OY 181 GTAKKNGTLYYMAPEHLNDVNAKPTKESDVYSFAVYLMAIFANKEPEYNAICEOQLIMC 240
Db 181 GTAKKNGTLYYMAPEHLNDVNAKPTKESDVYSFAVYLMAIFANKEPEYNAICEOQLIMC 240
OY 241 IKSNGRPDVIDITEYCPEIISLMKLCWEANPEAPPTFGIEKFRPYLSOLESEVED 300
Db 241 IKSNGRPDVIDITEYCPEIISLMKLCWEANPEAPPTFGIEKFRPYLSOLESEVED 300
OY 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATQPSLSHSGGLMGVPEESWFA 360
Db 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATQPSLSHSGGLMGVPEESWFA 360
OY 361 PSLEHPOEENEPSSLOSLODEANHYLHGSMDROTQKOPRONVAVNREERRRVSHPDF 420
Db 361 PSLEHPOEENEPSSLOSLODEANHYLHGSMDROTQKOPRONVAVNREERRRVSHPDF 420
OY 421 AQQRPYENFQTEKGYVSSASHGNAVHOPSGITSPQVLYONNGLYSHGCTRPDL 480
Db 421 AQQRPYENFQTEKGYVSSASHGNAVHOPSGITSPQVLYONNGLYSHGCTRPDL 480
OY 481 PGTAGPRVWYRPIPSHMPSLNIPVETNYLGNTPTMFSSLPPTDESIRKTIYNSTGIQ 540
Db 481 PGTAGPRVWYRPIPSHMPSLNIPVETNYLGNTPTMFSSLPPTDESIRKTIYNSTGIQ 540
OY 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYQAI FDNLTSLTKHLDPIENLGKHKMN 600
Db 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYQAI FDNLTSLTKHLDPIENLGKHKMN 600
OY 601 CARLIGFQSOIDIDHDYERDGLKEKYOMLOKWMVEGIGKATVGLAOLHOCSSRID 660
Db 601 CARLIGFQSOIDIDHDYERDGLKEKYOMLOKWMVEGIGKATVGLAOLHOCSSRID 660
OY 661 LLSLILYVSON 671
Db 661 LLSLILYVSON 671

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RESULT 8
AAW04627
ID AAW04627 standard; Protein: 656 AA.

AAW04627;
13-FEB-1997 (first entry)

Mouse receptor interacting protein.

Receptor interacting protein: RIP; cell death: apoptosis;
Fas; APO-1; signal transduction; cancer; gene therapy.

Mus sp.

Location/Qualifiers
1..300

Label= kinase_domain
/note= "N-terminal kinase domains extends from
a few residues after the N-terminal
Met residue to approx. residue 300"

Domain 557..656
/Label= Death_domain
/note= "the death domain covers the 98
C-terminal amino acid residues of RIP"

(W09636730-A1)

21-NOV-1996.

18-APR-1996; 96WO-US05386.

18-MAY-1995; 95US-044005.

(GENO) GEN HOSPITAL CORP.

(HARD) HARVARD COLLEGE.

Kim E, Leder P, Lee T, Seed B, Stranger BZ;

WPI: 1997-012106/01.

N-PSDB: AAT43752.

Receptor interacting protein having death and kinase domain - useful
to control diseases that involve abnormal apoptosis, and for
diagnosis and drug screening

Claim 5; Page 39-41; 64pp: English.

Mouse receptor interacting protein (RIP) (AAW04627) has an N-terminal
kinase domain and a C-terminal death domain through which RIP
interacts with the Fas/APO-1 intracellular domain (ICD). RIP
overexpression leads to cell death. The RIP amino acid sequence
was deduced from a cDNA clone (AAT43752) isolated from a mouse thymus
cDNA library. The RIP can be expressed in transformed host cells.
It is used to screen for cpds. that inhibit RIP-dependent promotion
of apoptosis or that induce RIP expression and therefore apoptosis.
CC RIP and anti-RIP antibodies are also useful as diagnostic reagents..

Sequence 656 AA:

Query Match 68.4%; Score 2423.5; DB 18; Length 656;
Best Local Similarity 69.8%; Pred. No. 3.6e-189;
Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

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OY 1 MOPDMSLVNIMKSSDLESAELDSGGGKVSICFHRQGLIMKTIVKGPNCIEHNEAL 60
Db 1 MOPDMSLVNIMKSSDLESAELDSGGGKVSICFHRQGLIMKTIVKGPNCIEHNEAL 60
OY 61 LEEAKMNRRLRHSRVKLVGLVIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSYGRITL 120
Db 61 LEEAKMNRRLRHSRVKLVGLVIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSYGRITL 120
OY 121 EIIEGMCLHKGKVIHDKLPENILVNDPFHRIKIDGLASFWMKSKLNNEEHNELREVD 180
Db 121 EIIEGMCLHKGKVIHDKLPENILVNDPFHRIKIDGLASFWMKSKLNNEEHNELREVD 180
OY 181 GTAKKNGTLYYMAPEHLNDVNAKPTKESDVYSFAVYLMAIFANKEPEYNAICEOQLIM 239
Db 181 GTAKKNGTLYYMAPEHLNDVNAKPTKESDVYSFAVYLMAIFANKEPEYNAICEOQLIM 239
OY 241 IKSNGRPDVIDITEYCPEIISLMKLCWEANPEAPPTFGIEKFRPYLSOLESEVED 300
Db 241 IKSNGRPDVIDITEYCPEIISLMKLCWEANPEAPPTFGIEKFRPYLSOLESEVED 300
OY 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATQPSLSHSGGLMGVPEESWFA 360
Db 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATQPSLSHSGGLMGVPEESWFA 360
OY 361 PSLEHPOEENEPSSLOSLODEANHYLHGSMDROTQKOPRONVAVNREERRRVSHPDF 419
Db 361 PSLEHPOEENEPSSLOSLODEANHYLHGSMDROTQKOPRONVAVNREERRRVSHPDF 419
OY 421 AQQRPYENFQTEKGYVSSASHGNAVHOPSGITSPQVLYONNGLYSHGCTRPDL 479
Db 421 AQQRPYENFQTEKGYVSSASHGNAVHOPSGITSPQVLYONNGLYSHGCTRPDL 479

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DR N-PSDB: AAS80491.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 20: SEQ ID No 46663; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 948 AA:

Query Match 43.1%; Score 1529; DB 22; Length 948;

Best Local Similarity 59.4%; Pred. No. 9.9e-116;

Matches 340; Conservative 31; Mismatches 95; Indels 106; Gaps 16;

QY 1 MOPMSLVNFKMSDFLESALDSCGFGKYSLCFHRQGLIMIKTVYKKGNCIEHNAL 60
DB 412 MOPMSLVNFKMSDFLESALDSCGFGKYSLCFHRQGLIMIKTVYKKGNCIEHNAL 471
QY 61 LEEAKMNRRLHSHSVKLLGVIIIEGKYSLVMEYMEKGNLHVLAKESTPLSVYGRITL 120
DB 472 LEEAKMNRRLHSHSVKLLGVIIIEGKYSLVMEYMEKGNLHVLAKESTPLSVYGRITL 531
QY 121 EIIIGMCTYHKGKVIHDKPENTLVNDPHIKTA----- 155
DB 532 EIIIGMCTYHKGKVIHDKPENTLVNDPHIKMSTPLSVYGRITL EIIIGMCTYHKGKV 591
QY 156 ---DLGLAS-----FKMKSILNNEHNEHLEVDGAKKNGGTLVYMAPEHLNDVAK 204
DB 592 IHRKLKPENLIVNDPHIKMKSILNNEHNEHLEVDGAKKNGGTLVYMAPEHLNDVAK 651
QY 205 PTERKSDVYSFAVNLMAIFANKEPEYNAICFQOLIMCISGRNRPVDITTEKCPREITSLM 264
DB 652 PTERKSDVYSFAVNLMAIFANKEPEYNAICFQOLIMCISGRNRPVDITTEKCPREITSLM 711
QY 265 KLCHEANDEARPTTP-----GIEEKFRPPYLSQLESVEEDYKSLAKETSN 310
DB 712 KLCHEANDEARPTTP-----GIEEKFRPPYLSQLESVEEDYKSLAKETSN 771
QY 311 ENAVVAKMOSLQDLCVAVPSSR--SNSATQPSGLSHSSQGLMGVSESWFAPSLHPOE 368
DB 772 HLVTAEKLP-----AARNRRAPTCCTSEPOSAVLPH---LGAER---LPA--PRN 816
QY 369 ENEPISLOSLQDEANVHLVSGRMDRQTKQOPRONAVYAREERRRVSHDPAOORPYEN 428
DB 817 RRAPTCCTSEPOSAVLPH---LGAER---LPA--PRN 865
QY 429 FQNTGEGCTVYSSAASHGNVHOPSGLSLPOVLYONNGLYSSHGFGRLPDG----- 482
DB 866 -----LGTAEKLPAAAPNR--RAPTCCTSEPOSAVLPH-----LGTAAKLPAAAPNR 911

QY 483 -----TAGPRVWRPSPHMSPLHNIPVETN 509
DB 912 APTCCTSEPOSAVLP---HLGTAAKLPAAAPSN 940

RESULT 11

AAB01524

ID AAB01524 standard; Protein; 518 AA.

AC AAB01524;

DT 08-NOV-2000 (first entry)

DE Kinase of death (KOD).

XX KOD: kinase of death; programmed cell death; apoptosis; cancer;
XX autoimmune disease; stroke; Alzheimer's disease; identification.

OS Homo sapiens.

PM US6096539-A.

PD 01-AUG-2000.

PF 10-JUN-1999; 99US-0329418.

PR 10-JUN-1999; 99US-0329418.

PA (ZENE) ZENECA LTD.

PI Gomes BC, Prosser JC, Kasof GW;

DR WPI: 2000-523872/47.

DR N-PSDB: AAA47701, AAA47702.

PT New nucleic acids encoding a protein activator of apoptosis for
PT preventing, diagnosing and treating pathophysiological disorders
PT related to apoptosis

PS Claim 1: Columns 33-36; 32pp; English.

CC The kinase of death (KOD) polypeptide is integral to the activation
CC process of cellular apoptosis (programmed cell death). Apoptosis is
CC needed to orchestrate biological maintenance of an organism during
CC development as well as to preserve the normal function and fitness of
CC tissues during a normal life span. Physiological conditions which
CC result from aberrant apoptosis may be dire. Cancer and autoimmune
CC disease may result when there is too little apoptosis as well as
CC severe stroke damage or the neurodegeneration of Alzheimer's disease
CC when there is too much apoptosis. The KOD polypeptide is useful for
CC studying pathophysiological disorders related to apoptosis as well
CC as for identifying compounds that modulate biological and/or
CC pharmacological activity of the native mediator of apoptosis.

SQ Sequence 518 AA:

Query Match 12.2%; Score 433; DB 21; Length 518;

Best Local Similarity 25.5%; Pred. No. 1.8e-26;

Matches 146; Conservative 96; Mismatches 184; Indels 146; Gaps 22;

QY 14 SSDFLESALD--DSGFGKYSLCFHRQGLIMIKTVYKKGNCIEHNALLEEAKMNRRLH 72
DB 17 STEELNENLVKGGGFGTVFRAQRHKG-----YDAVAIVNSKALSREYKAMASLDN 69
QY 73 SRVYKLLGVI-----IEGKYSLVMEYMEKGNLHVLAKESTPLSVYGRITL EIEGMC 127
DB 70 EFVALRTEGVIEKVNMDQPKPALVTKFMENGSLSGLSQCPRPWPLLCRLLEKVLGME 129
QY 128 VYHKGK--VTHKDKPENTLVNDPHIKIADGLASFMSKSKLNNEHNEHLEVDGTA 184
DB 130 YLHDQNPVLLHRLDKPSNVLLDPELHVLADEGLSTFGGSG-----SGTSG 177
QY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVNLMAIFANKE---PYE-----NAICQ 236

FT Misc-difference 112 decoding with AAD16312"
 FT /note- "Encoded by YGG; This occurs while decoding
 FT with AAD16313"
 FT 280..518
 FT Domain /note- "Death domain"
 FT US6267956-B1.
 PD 31-JUL-2001.
 XX
 XX 21-MAR-2000; 2000US-0531914.
 PF
 XX 10-JUN-1999; 99US-0329418.
 PR
 XX (ZENEC) ZENECA LTD.
 PA
 XX Gomes BC, Kasof GM, Prosser JC;
 XX
 XX WPI: 2001-535022/59.
 DR N-PSDB: AAD16312, AAD16313.
 XX
 XX New human protein activator protein, useful for treating dysfunctional
 PT apoptosis conditions and in screening assays to identify agonists which
 PT agonize or mimic biological and/or pharmacological activity -
 XX
 PS Claim 1; Column 33-36; 31pp; English.
 XX
 XX The invention relates to human protein activator of apoptosis and
 CC methods to identify compounds that modulate the biological and/or
 CC pharmacological activity of the activator and hence regulate
 CC apoptosis. The nucleic acid and amino acid sequences of the kinase
 CC of death (KOD) are useful for identifying compounds that modulate
 CC the biological and/or pharmacological activity of a native mediator
 CC of apoptosis, for treating dysfunctional apoptosis conditions, in
 CC screening assays to identify agonists which agonize or mimic
 CC biological and/or pharmacological activity, induce production of or
 CC prolong the biological half-life of the molecule in vivo or in vitro.
 CC The present sequence is human KOD protein activator of apoptosis.
 CC
 XX
 SO Sequence 518 AA:
 Query Match 12.2%; Score 433; DB 22; Length 518;
 Best Local Similarity 25.5%; Pred. No. 1.8e-26;
 Matches 146; Conservative 96; Mismatches 184; Indels 146; Gaps 22;
 OY 14 SSDFLSAEL-DSGFGKVSICFHRTGOLMIMTKVYKGPNCIEHNEALLEEAKMNRRLRH 72
 DB 17 STELENOELVKGKGFVFRAGHRKMG-----YDAVAVIVSKAISREVKAMASLDN 69
 OY 73 SRVYKLGVI-----IEGKSYLMEYMEKGNLMHVLAKESTPLSYKGRITILEIGMC 127
 DB 70 EYVRLTEGVLEKVMWDDPKPALVTYKTEMENGLSGLLQSOQPRWPLCLRLKEVILGMF 129
 OY 128 YLHKGK--VIHKDKPENILVNDNFHFKIADLGLASFPMKSLNNEHEHNELEVDGAK- 184
 DB 130 YLHQNQNVLLHRDLAKPSNVLLDPELHKLADFGISTGQSGQ-----SGHSG 177
 OY 185 KNGSTLYMADEHLNDVNAKPTESDYVSFAVLAIAFANKE---PYE-----NAICEQ 236
 DB 178 EPGGTLLGYLAPLELVNNAKASTASDVSEGLIMAVLAGREVELPEPSLVYAVACNRQ 237
 OY 237 LIMIKSGNRPDVDITIEYCPRE-----IISLMKLCHEANPEARTF---PGIEKFRP 287
 DB 238 -----NRPSTLAEPLQAGEETPGLEGLEKELMQLCWSSEKDRPSFOECLPKTDEVFQ- 288
 OY 288 FYLSQLEESVEEDVKSILKEYSNENAVVKKRMOSQLQDCAVAPSSRSNSATQPSLSHSQ 347
 DB 289 -----MVENNNAANASTYKVDLSQARSSNRF-----STPES----- 320
 OY 348 GLGKGPVYESWFAFSLSEHPOEENEPSSLOSKLODEANYHLVGSRMDRQTKOQRONVAVNR 407
 DB 321 --GCGGTETMDGFRRTIENQHSRNDVAVSEML-----NKLLEEPSPSSVDPK 365

OY 408 EE-ERRRRVSHDPFAQQRPEYENFQNTBEKGTIVYSSASHGNAVHQPSTLSQPOVLYONN 466
 DB 366 PSLTKRSRAQEDQVPA-----WAGTSSSQMKAP--POTPETSTFRN 406
 OY 467 GLYSHGFGTGPLDGTAGPRVWYRPPIPSHMPSLHNIPEPTNYLGNTPTPFPSSLPPTD 526
 DB 407 QMPS-----PTSTGCT-----PS-----GPRGNGCAERQGNMNSCRTPPEP 441
 OY 527 ESIR-----YTIYNSTGIGIAYNWEIGTSS 554
 DB 442 NPVTGRPLVNIYNCSGVQVGDNNYLTMOQTFA 473
 RESULT 14
 AAE09432
 ID AAE09432 standard; Protein; 518 AA.
 XX
 AC AAE09432;
 XX
 DT 19-NOV-2001 (first entry)
 XX
 DE Human kinase of death (KOD) dominant negative mutant, K50R.
 XX
 KW Human: protein activator; apoptosis; kinase of death; KOD; therapy;
 KW cytosolic; mutant; mutein.
 OS
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN US6267956-B1.
 XX
 PD 31-JUL-2001.
 XX
 PF 21-MAR-2000; 2000US-0531914.
 XX
 PR 10-JUN-1999; 99US-0329418.
 XX
 PA (ZENEC) ZENECA LTD.
 XX
 XX Gomes BC, Kasof GM, Prosser JC;
 XX
 XX WPI: 2001-535022/59.
 DR
 XX
 PT New human protein activator protein, useful for treating dysfunctional
 PT apoptosis conditions and in screening assays to identify agonists which
 PT agonize or mimic biological and/or pharmacological activity -
 XX
 PS Disclosure; Column 37-40; 31pp; English.
 XX
 XX The invention relates to human protein activator of apoptosis and
 CC methods to identify compounds that modulate the biological and/or
 CC pharmacological activity of the activator and hence regulate
 CC apoptosis. The nucleic acid and amino acid sequences of the kinase
 CC of death (KOD) are useful for identifying compounds that modulate
 CC the biological and/or pharmacological activity of a native mediator
 CC of apoptosis, for treating dysfunctional apoptosis conditions, in
 CC screening assays to identify agonists which agonize or mimic
 CC biological and/or pharmacological activity, induce production of or
 CC prolong the biological half-life of the molecule in vivo or in vitro.
 CC The present sequence is a dominant negative mutant of human KOD
 CC protein activator of apoptosis. The lysine at position 50 of native
 CC KOD is changed to arginine in the mutant sequence.
 CC
 XX
 SO Sequence 518 AA:
 Query Match 12.2%; Score 433; DB 22; Length 518;
 Best Local Similarity 25.5%; Pred. No. 1.8e-26;
 Matches 146; Conservative 96; Mismatches 184; Indels 146; Gaps 22;
 OY 14 SSDFLSAEL-DSGFGKVSICFHRTGOLMIMTKVYKGPNCIEHNEALLEEAKMNRRLRH 72
 DB 17 STELENOELVKGKGFVFRAGHRKMG-----YDAVAVIVSKAISREVKAMASLDN 69

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 25, 2003, 20:27:10 ; Search time 2042 Seconds

(without alignments)
5321.827 Million cell updates/sec

Title: US-09-981-397A-16

Perfect score: 3545

Sequence: 1 MOPDMSLVNKKMSDFLES.....ALHQCRIIDLSLLIVSQN 671

Scoring table:

BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delpop 6.0 , Delpext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n model -DEV=xlp

-Q/cgnt2.1/USFTO.spool/US09981397/runat_21062003_134007_18444/app-query.fasta.1.839

-DB-EST -OPM=fastap -SUFTX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0

-UNITS-bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS-human40.cdi -LIST=45

-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFM=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USRR=US09981397.ecn.1.1.2874.etrnat_21062003_134007_18444 -NCRU=6 -ICPU=3

-NO_MAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *

1: em_estba:*

2: em_esthum:*

3: em_estinu:*

4: em_estinu:*

5: em_estlov:*

6: em_estlo:*

7: em_estro:*

8: em_estro:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est5:*

15: em_estfun:*

16: em_estfun:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vit:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1528	43.1	869	9	AL521376	AL521376 AL521376
2	1470	41.5	971	9	AL545479	AL545479 AL545479
3	1278.5	36.1	14	14	B0962541	B0962541 AGENCOURT
4	1222	34.5	732	9	AU140586	AU140586 AU140586
5	1205	34.0	894	13	B1257769	B1257769 602969751
6	1158	32.7	672	9	AL704842	AL704842 DKFZP686C
7	1156.5	32.6	812	12	BE884263	BE884263 601505730
8	1142.5	32.2	719	12	BG107606	BG107606 602277759
9	1102	31.1	656	14	BQ317122	BQ317122 QVO-CT038
10	1028	29.0	960	14	BQ647524	BQ647524 AGENCOURT
11	1019.5	28.8	775	13	B1663126	B1663126 603266738
12	979.5	27.6	805	13	B1559218	B1559218 603240839
13	884	24.9	649	12	BG691740	BG691740 341033 BA
14	870	24.5	563	10	AW890282	AW890282 MRO-NT003
15	864.5	24.4	786	12	BG387238	BG387238 602455976
16	850	24.0	484	9	AL039269	AL039269 DKFZP7270
17	746	21.0	663	10	BE573589	BE573589 60133617
18	735	20.7	500	12	BG689507	BG689507 337612 BA
19	691	19.5	444	10	BE001662	BE001662 PMO-BN008
20	689	19.4	693	12	BF055235	BF055235 7177412.x
21	681	19.2	674	10	BB616659	BB616659 BB616659
22	658.5	18.6	895	13	B1599131	B1599131 603246349
23	655	18.5	425	10	AW236421	AW236421 XM64606.x
24	648	18.3	552	12	BE756621	BE756621 210812 MA
25	639	18.0	1028	9	AL571266	AL571266 AL571266
26	635	17.9	942	10	BE285518	BE285518 601096893
27	633	17.9	385	12	BF086124	BF086124 CM2-GN005
28	627.5	17.7	409	12	BF737966	BF737966 CM2-KT003
29	625.5	17.6	585	13	BM191199	BM191199 d8133310
30	589	16.6	574	9	AA271576	AA271576 VB77407.r
31	572	16.1	707	9	AJ455969	AJ455969 AJ455969
32	493	13.9	893	13	B1331833	B1331833 602982511
33	488.5	13.8	670	13	BJ000439	BJ000439 BJ000439
34	459	12.9	310	9	A1801478	A1801478 t089h04.x
35	455	12.8	506	10	AW433969	AW433969 UT-R-BJ07
36	436	12.3	323	10	AW353174	AW353174 34902 MAR
37	430	12.1	728	9	AL521375	AL521375 AL521375
38	424	11.7	483	14	BE381822	BE381822 601272355
39	414	10.9	231	14	BQ780368	BQ780368 UT-R-FFO
40	388	10.9	231	14	Z45688	Z45688 HSCZRE091.n
41	373	10.5	732	12	BE898370	BE898370 601681196
42	370	10.4	349	9	A1338106	A1338106 q106b01.x
43	354	10.0	1051	12	BF783377	BF783377 602110215
44	340.5	9.6	305	9	AA143087	AA143087 z069b11.r
45	338.5	9.5	2046	11	AK013606	AK013606 Mus muscu

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	869 bp	MRNA	linear	EST 13-FEB-2001
AL521376	AL521376	AL521376 LTL_NF1004_NBC2 Homo sapiens CDNA clone CSDB0001YF10.5				
AL521376	AL521376	prime, mRNA sequence.				
ACCESSION	AL521376	GI:12784869				
VERSION	AL521376.1	GI:12784869				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.					
TITLE	Full-length cDNA libraries and normalization					


```

Oy 56 HisAsnGluAlaLeuLeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgVal 75
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Db 71 CACACAGCAGGSCCTCTGGAGGAGGCGCAAGATGATGACACACTGAAACACAGCCGGGTG 130
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Oy 76 ValLysLeuLeuGluValLleIleGluGluGlyLysTyrSerLeuValMetGluTyrMet 95
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Db 131 GTGAGGCTCTGGGCGCATCATCATGAGAGGAAAGTACTCCGCTGGATGAGTACATG 190
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Oy 96 GluLysGluLysLeuMetHisValLeuLysAlaGluMetSerThrProLeuSerValLys 115
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Oy 256 CysProArgGluIleIleSerLeuMetLysLeuCysTyr-GluAlaAsnProGluAlaArg 275
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Oy 275 gProThrPheProGlyIleGluGluLysPheArgProPheTyrLeuSerGluLeuGluGlu 295
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Db 730 GCCGACATTTCTGCGCATGTGAAGAAATTTAGGCCCTTTTATTTAAGTCAATTAGAGA 789
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Oy 295 uSerValGluGluAspValLysSerLeuLysGluTyrSerAsnGluAsnAlaValAla 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 790 AAGTGTAGAGAGAGACCTGAAAGAGTTTAAAGAAAGATATTCAACAAACAAATGAGTGT 849
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Oy 315 LysArgMetGlnSerLeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSe 335
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Oy 335 ValAlaThrGluGlnProGlySerLeuHisSerSerGluGlyLeuGlyMetGlyProValG1 355
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Db 910 AGCCACAGAACAGACT-GGTTCACTGACACAGTTCACAGGACTTGGGATGGGCKCTGGGA 968
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Oy 355 u 355
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Db 969 G 969
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```

```

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 931)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Gene distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LCM2564 row: d column: 04
High quality sequence start: 30
High quality sequence stop: 584.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6378579"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
BASE COUNT 290 a 196 c 245 g 200 t
ORIGIN
Alignment Scores:
Pred. No.: 1,59e-129 Length: 931
Score: 1278.50 Matches: 271
Percent Similarity: 89.84% Conservative: 12
Best Local Similarity: 86.03% Mismatches: 13
Query Match: 36.06% Indels: 19
DB: 14 Gaps: 5
US-09-981-397a-16 (1-671) x BQ962541 (1-931)
Oy 84 GluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisVal 103
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Db 13 GAGCAGGGGAGACATGCA-----GAAGGGAACCTGATGCAGCTG 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 104 LeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeuGluIleLe 123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 52 CTGAAGCCGAGAGAGACTCCGCTTCTGTAAAGGAAGATTAATTTTGAATCATTT 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 124 GluLysMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysProGluAsn 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 112 GAAGGATGTGCTCTTAAATGATGAGAAAGCGCTGATACAGAGACCTGAAGCCGTAAT 171
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 144 IleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLys 163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 172 ATCTTGTGATATGACTTCCACATTAAGATCCAGACCTCGGCTTGCTCTTAAG 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 164 MetTyrSerLysLeuAsnGluGluHisAsnGluLeuArgGluValAspGlyThrAla 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 232 ATGTGAGCAACATGAATTAATGAGAGACACATAGCTGAGAGAGTGGACGCGCT 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 184 LysLysAsnGlyLysThrLeuTyrTyrMetAlaProGluHisLysAsnAspValAsnAla 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 AAGAGAAATGGCGGACCGCTCTACTACTGCGCGCGGCGAGACCTGATGAGTCAACGCA 351
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OY		204	LysProthrGluLysSerAspValTyrSerPheAlaValIalleuTrpaIallepheala	223
Db		352	AAGCCACAGAGAAGTCGGATGTGTACACTTTGGCTGTAGTCTCGGCCGATATTGGA	411
OY		224	AsnLysGluProTyrGluasnAlalleCysGluIngnLeuIlleMetCysLleLysSer	243
Db		412	AATAAAGAACCATATGAANAATCTATCTGTGACGACAGCAATTATGTATGCAATAAATT	471
OY		244	GlyAsnArgProAspValAspaspIleThrGluTyrCysProArgGluIleLeuSerLeu	263
Db		472	GGCAACAGGCAGATGTGGATGACATCACTGTAGTCTGCCCAAGAAGAAATTTCAGTCTC	531
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Db		532	ATGAAGCTCTGCTGGGAAGCCGAATCCGGAAGCTCGCCGACATTTCTCGGCAWTGAACA	591
OY		284	-LysPheArgProPheTyrLeuSerGluLeuGluGluSerValGluGluAspValLysLe	303
Db		592	AAAAATTTAGCCTTTTATTATTAAGTCATTTAGAGAAGAGTGTAAGAAGACGTGAAGAG	651
OY		303	IleuLysLysGluTyrSerAsnGluAsnAlaValAl-lysArgmetGlnSerLeuGlnL	323
Db		652	TTTAAGAAGAGCATATCAAAGAAATGCACTGTGGAAAAGATGCACTGCTCTTCAAC	711
OY		323	euaScCyS-ValAlaVal-ProserSerArgserAsnSerAlaThrGluInProGlySe	342
Db		712	TGATTTGGGGGTGGCCATCCCTTCAAGCGGGTCAAAATTGACCACAGAAACCTGTGTTT	771
OY		342	IleuHisSerSer-GlnGly-LeuGlyMetGlyProVal---GluGluSerTrp--Phe	359
Db		772	CCTGCACAGTTGCCCAAGGAGACTTGGGATTTGGGCTGTGTGGAGAAGAACCCGTGGTTGG	831
OY		360	AlaProSer-LeuGluHisProGlnGlu---GluAsnGluProSerLeuGlnSerLysLe	378
Db		832	CTCCCTTCCC GGCGAGCACCCCCAGAAAAGAAATGAGCCAGCCTGTGCGAGAGAAAC	891
OY		378	u---GlnaspGluAlaAsn-TyrrHisLeu 386	
Db		892	CTCCAAAACGAGGCCACTTACCTT 920	
RESULT 4				
LOCUS	AUI40586	732 bp	mRNA	linear EST 05-AUG-2002
DEFINITION	AUI40586 PLACE3 Homo sapiens cDNA clone PLACE3000347 5', mRNA			
ACCESSION	AUI40586			
VERSION	AUI40586.1	GI:11002107		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 732)			
AUTHORS	Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuno,Y., Saito,K., Ishii,S., HRI human cDNA Project (Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuno,Y., Isogai,T.)			
TITLE	Unpublished (2000)			
JOURNAL	Contact: Takao Isogai			
COMMENT	Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1..732			
FEATURES				
source				

BASE COUNT	226 a	150 c	189 g	164 t	3 others
ORIGIN					
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Percent Similarity:	97.13%	Conservative:	2		
Best Local Similarity:	96.31%	Mismatches:	7		
Query Match:	34.47%	Indels:	1		
DB:	9	Gaps:	0		
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QY	129	LeuHISGLYSGLYValIIHeHISLysASPLLeuLysProGluAsnIleLeuValAspAsn	148		
Db	2	GTACATGGAAGGCGGTGATACCAAGACACCTCGAAATATCTCTGTGATAT	61		
QY	149	AspPheHISLLeuLysIIeAlAspLeuGlyLeuAlAspPheLysMetTrpSerLysLeu	166		
Db	62	GACCTCCACATTAAGATCCAGACCCCGGCTCTGCTCTTAAGATGTGGAGCAACTG	121		
QY	169	AspAsnGluGluHISAsnGluLeuAArgGluValAspGlyThrAlaLysLysAsnGly	188		
Db	122	AAATATCAAGACACATGAGCTGAGGCAAGTGGACGGCACCGCTTAAGAGAAATGGCGGC	181		
QY	189	ThrLeuTrpTrpMetAlaProGluHISLeuAspValAsnAlaLysProThrGluLys	208		
Db	182	ACCCTTACATACATGGCGCCGACGACCTGATGACGTCAACGCCAAGCCACAGAGAG	241		
QY	209	SerAspValLysSerPheAlaValAlaLeuTrpAlaIlePheAlaAsnLysGluProTyr	228		
Db	242	TCCGATGTGTACAGCTTCTCTGTAGACTGTGGCGATATTTGCAAAATAGACCCATAT	3010		
QY	229	GluAsnAlaIleCysGluGlnGluLeuIleMetCysIleLysSerGlyAsnArgProAsp	248		
Db	302	GAAATATGCTATCTGTAGACGACAGTTGATTAATGTCATAAATCTGGGAACAGGCCAGAT	361		
QY	249	ValAspAspIleThrGluTyrCysProArgIleIleSerLeuMetLysLeuCysTrp	268		
Db	362	GTGATGACATCTGACAGTACGCCCAAGAAATATACAGTCTCAATGAAAGCTCTGATGG	421		
QY	269	GluAlaAspProGluAlaArgProThrPheProGlyIleGluGluLysPheArgProPhe	288		
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QY	289	TyrLeuSerGlnLeuGluGlnuSerValGluGluAspValLysSerLeuLysLysGluTyr	308		
Db	482	TATTTTAAGCAATTAAGAAAGAGTGTAGAAGAGGAGCGTAAGAGATTAAAGAAAGATAT	541		
QY	309	SerAsnGluAspAlaValAlaLysArgMetGlnSerLeuGlnLeuAspCysValAlaVal	328		
Db	542	TCAAAAGCAAAATGCACTGTGGAAGCAATGCAAGTCTTCAACTGATTTGTGCGCAGTA	601		
QY	329	ProSerSerArgSerAsnSerAlaThrGlnGlnProGlySerLeuHISSerSerGlnGly	348		
Db	602	CCTTAAGCGCGGTCAATTCACGCCACCAAGACCTGGTTCACTGCACAGATTTCCANGCA	661		
QY	349	LeuGlyMetGlyProValGluGluGlnSerTrpPheAlaProSerLeuGlnHISProGlnGlu	368		
Db	662	CTTGGATGGGTCCTGTGGANGAGCTCGGGTCTCTTCCCTTCCGTGGAGCACCCACA-GAA	720		
QY	369	GluAsnGluPro 372			
Db	721	GAGATGACCCA 732			

LOCUS B1257769 894 bp mRNA linear EST J17-JUL-2001
 DEFINITION 60296975J1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109133 5',
 mRNA sequence.
 ACCESSION B1257769
 VERSION B1257769.1 GI:14813469
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 894)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMD at:
 http://image.lnl.gov
 Plate: LMD1264 row: f column: 14
 High quality sequence stop: 738.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5109133"
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 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 BASE COUNT 275 a 228 c 203 g 188 t
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 Alignment Scores:
 Pred. No.: 1..8e-121 Length: 894
 Score: 1205.00 Matches: 244
 Percent Similarity: 94.98% Conservative: 2
 Best Local Similarity: 94.21% Mismatches: 5
 Query Match: 33.99% Indels: 8
 DB: 13 Gaps: 0
 US-09-981-397a-16 (1-671) x B1257769 (1-894)
 Oy 302 LysSerLeuLysLysGluTyrSer-AsnGluAsnAlaValAlaValysArgMetGlnSerLe 321
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 Db 2 AAGAGTTTAAAGAAAGAGTATCAATACGAAATGCACTTGTGAAGAAATGCACTCTCT 61
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 Oy 321 uGluLeuAspCysValAlaValaProSerSerArgSerAsnSerAlaThrGluGlnProG 341
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 Db 62 TCAACTGATATGTGTGGCAGTACTTCAAGCCGGTCAATATTCAGCACAGAACACCTGG 121
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 Oy 341 ySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGlnSerTTPheAlaPr 361
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 Db 122 TTCACGTGACAGTTCGCCAGGACCTGGGATGGGCTCTGTGAGAGAGTCTGTTGGCTCC 181
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 Oy 361 oSerLeuGlnHisProGlnGluGlnGluAsnGlu-ProSerLeuGlnSerLysLeuGlnAspG 381
 |||||||
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 |||||||
 Oy 381 LuAlaAsnTyrHisLeuTyrGlySerArgMetAspArgLThrLysGlnGlnProArgG 401
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 Db 242 AAGCACTACCATCTTTATGCGACCCCATGAGACAGCAGACAAACAGACACCCCAAC 301
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 Oy 401 InAsnValAlaTyrAsnArgLugluGlu-ArgArgArgArgValSerHisAspProPhe 420
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Oy 421 AlaGlnGlnArgProTyrGluAsnPhesInasnthrgluGlyLysGlyThrValTyrSer 440
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 Oy 521 SerLeu-Pro-ProThrAspGlnSerIleLysTyrThr-IleTyrAsnSerThrGlyLe 539
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 Db 662 TCTTGACACCAACCAAGATGATATATATATGAGCTGGGGAGCC 721
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 Db 722 CAGATTGAGCTTACATTAATTTGAGCTGGGGAGCC 762
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 AL704842
 LOCUS DKFZP686C1633.r1 686 (synonym: hicc3) Homo sapiens cDNA clone
 DKFZP686C1633 5', mRNA sequence.
 AL704842
 ACCESSION AL704842.1 GI:19688197
 VERSION AL704842
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 672)
 Wiemann, S., Obermaier, B., Mewes, W., Mewes, H.W., Weill, B. and Wiemann
 EST (Ottewaelde, B., Obermaier, B., Mewes, H.W., Weill, B. and Wiemann
 'S.,)
 Unpublished (2001)
 JOURNAL Contact: Ottewaelde B
 COMMENT MIPS
 Am Klopferspitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by MediGenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project. No sl sequence
 available.
 This clone (DKFZP686C1633) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 FEATURES
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 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"
 BASE COUNT 206 a 157 c 170 g 137 t 2 others
 ORIGIN

Alignment Scores:

Pred. No.: 1,62e-116 Length: 672
 Score: 1158.00 Matches: 219
 Percent Similarity: 98.21% Conservative: 4
 Best Local Similarity: 98.21% Mismatches: 0
 Query Match: 32.67% Indels: 0
 DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x AL704842 (1-672)

OY 262 SerleuMetLysLeuGlySerArgMetLysPheGlnValAlaValProGlnPheProGlyLeu 281
 DB 2 AGCTTCAGGAAGCTCTGCTGGCAACCGAATCCGGAACTCCGCCACATTTCTGGCATT 61
 OY 282 GluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspAla 301
 DB 62 GAAGAAAATTAGGCCCTTTTATTATTAGTCAATTAGAGAAAGTGTGAAGAGAGAGAGCTG 121
 OY 302 LysSerLeuLysGlyTyrSerAsnGluAsnAlaValAlaLysArgMetGlnSerLeu 321
 DB 122 AAGAGTTAAAGAAAGACTATTCAACGAAATGACAGTTGTGAAGAGAAAGAGAGCTCTT 181
 OY 322 GlnLeuAspGlyValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProGly 341
 DB 182 CAACCTGATTTGTTGGCAGTACCTTCAACCGCTCAAAATTCAGCCACAGAACAGCCTGCT 241
 OY 342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTyrPheAlaPro 361
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 OY 362 SerLeuGlnHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGlu 381
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 DB 362 GCCAACTACACATCTTTATGAGCGCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
 OY 402 AsnValAlaTyrAsnArgGluGluGluArgArgValSerHisAspProPheAla 421
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 DB 542 GCACCCAGTCTGATATGAGTGCACAGCCCTCAGGCTCACCAGCCCACTCAAGTA 601
 OY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
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 DB 662 GGAACACGA 670

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 DEFINITION 601505730F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907350 5',
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 ACCESSION BE884263
 VERSION BE884263.1 GI:10333039
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 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 812)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs.rem@nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMN at:

<http://image.llnl.gov>
 Plate: LAM9717 row: 1 column: 07
 High quality sequence stop: 633.

FEATURES

source

1..812

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/db_xref="taxon:9606"

/clone_image="IMAGE:3907350"

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/tissue_type="telomysarcoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-Sport6; Site: 1; NCI; Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dt.

Average insert size 2.1 kb.

BASE COUNT 259 a 195 c 190 g 168 t

ORIGIN

Alignment Scores:

Pred. No.: 3.28e-116 Length: 812
 Score: 1156.50 Matches: 225
 Percent Similarity: 93.52% Conservative: 6
 Best Local Similarity: 91.09% Mismatches: 11
 Query Match: 32.62% Indels: 5
 DB: 12 Gaps: 1

US-09-981-397a-16 (1-671) x BE884263 (1-812)

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 DB 3 CATGACCTCTTTGGACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 62
 OY 437 ThrValTyrSerSerAlaIleSerHisGlyAsnAlaValHisGlnProSerGlyLeuThr 456
 DB 63 ACTGCTATATTCAGTGCAGCCAGTCAAGTATGATGACAGTGCAGCCAGCCCTCAGGCTCACC 122
 OY 457 SerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThr 476
 DB 123 AGCCAACTCTAAGTACTGATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 182
 OY 477 ArgProLeuAspProGlyThrAlaGlyProArgValTyrPyrArgProIleProSerHis 496
 DB 183 AGACCACTGGATCCAG 242
 OY 497 MetProSerLeuHisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThr 516
 DB 243 ATGCTAGTCTGATATATCCAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 302
 OY 517 MetProPheSerSerLeuProProThrAspGlnSerIleLysTyrThrIleTyrAsnSer 536
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 OY 537 ThrGlyIleGlnIleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeu 556
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 DB 423 CTAGACAGACCAAAATACGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
 OY 577 AspAsnThrThrSerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLys 596
 DB 483 GATATATCCACTATCTGAG 542
 OY 597 HisTrpLysAsnGlyAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGlnIleAla 616

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Db 543 CACGGGAAAACTGTCGCCGTAACCTGGGGCTTCACACAGCTCAGATTGATGAAATG 602
OY 616 SPHSASPTYGLIARASpGLYLeuLYSGIuLYSValTYR---GImetLeuGlnIYST 635
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Db 603 ACCATGCTTATGACCGAGATGACTGGAAAGAGAGATTACAGAAATGCTCCAAAGT 662
OY 635 rp-ValMet-ArgGluGlyIleLYSGIAlaThrValGlyLYSLeuAlaGlnAlaLeuH 654
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Db 663 GGGCTGATGACGGAACGATACAGGAGAGCCCGGTGGGGAAGAGCTGGCCAGGCTCC 722
OY 654 sGlnCySerArg 658
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Db 723 CCAATGTTCCAGA 735
RESULT 8
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LOCUS 602277759P1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4365327 5'
DEFINITION mRNA sequence.
ACCESSION Bg107606
VERSION Bg107606.1 GI:12601452
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 719)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@pds-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
Plate: LLM10014 Row: f Column: 16
High quality sequence stop: 693.
Location/Qualifiers
1..719
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4365327"
/clone_id="NIH_MGC_86"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: Nott;
Site_2: Salti. Cloned unidirectionally; oligo-dt primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT 241 a 171 c 159 g 148 t
ORIGIN
Alignment Scores:
Pred. NO.: 9.22e-115 Length: 719
Score: 1142.50 Matches: 230
Percent Similarity: 95.45% Conservative: 1
Best Local Similarity: 95.04% Mismatches: 8
Query Match: 32.23% Indels: 6
Db: 12 Gaps: 1
US-09-981-397a-16 (1-671) x Bg107606 (1-719)
OY 396 LysGlnGlnProArgGlnAsnValAlaIleTyrAsnArgGluGluGluArgArgArgVal 415
|||||
Db 2 AAACAGCAGCCCAACAGAGATGTGGCTTACACAGAGAGAGAGAGAGAGAGAGGTC 61
OY 416 SerHisAspProPheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLYS 435

|||||
Db 62 TCCCATGA-CCTTTGCACACAGCAAGACCTTACAGAAATTTTCAGAAATACAGAGGAAAA 120
OY 436 GlyThrValTYrSerSerAlaAlaSerHisGlySnaAlaValHisGlnProSerGlyLeu 455
|||||
Db 121 GGCACGTGTTATTCAGAGCGAGCGAGTCATGTGTAATGACAGCCACGCCCTCAGGGCTC 180
OY 456 ThrSerGlnProGlnValLeuTYrGlnAsnGlnGlyLeuTYrSerSerHisGlyPheGly 475
|||||
Db 181 ACCAGCCACCTCAAGTACTTATTCAGACATGATTAATATAGCTCAGATGGCTT-6GA 239
OY 476 ThrArgProLeuAspProGlyTYrAlaGlyProArgValTrrTYrArgProIleProSer 495
|||||
Db 240 ACAAGACACTGATGATCCAGAGCAAGACAGAGTCCAGAGT-TCGTACAGGCCAATCCAAAGT 298
OY 496 HisMetProSerLeuHisAsnIleProValProGluThrAsnTYrLeuGlyAsnThrPro 515
|||||
Db 299 CATATGGCTAGTGCATTAATATCCAGTGGCTCAGACCACTATCAGAAATACACCC 358
OY 516 ThrMetProPheSerSerLeuProProThrAspGlnSerIleLYSTYrThrIleTYrAsn 535
|||||
Db 359 ACCATGCCATTACACTCCCTTGCACACACAGATGAATCTATTAATATACCATATACAT 418
OY 536 SerThrGlyIleGlnIleGlyAlaTYrAsnTYrMetGluIleGlyGlyThrSerSerSer 555
|||||
Db 419 AGTACGTGCATTTAGATTGGAGCCTACATTAATGAGATTGGTGGAGAGTTCAATCA 478
OY 556 LeuLeuAspSerThrAsnThrAsnPhelYSGluGluProAlaAlaLYSTYrGlnAlaIle 575
|||||
Db 479 CTACTACACACACCAATATACGAACTCAAAAGAGCCAGCTGCTAGTACCAAGCTATTC 538
OY 576 PheAspAsnThrTrpThrSerLeuThrAspLYSHisLeuAspProIleArgGlu-AsnLeuG 595
|||||
Db 539 TTGATATATACCTAGCTAGCTGACGAGTAACACCTGGACCAATCAGGGAACATCTGGG 598
OY 595 YLYSHISTrp-LysAsnCysAlaArgLYSLeuGlyPheThrGlnSerGlnIleAspGlu 615
Db 599 AAACGACCTGGGAAAAAAGCTGCCGCTAACGAGGCTTCACACAGTTCAGATTATGAA 658
OY 615 LeAspHisAspTYrGluArgAspGLYLeuLYSGIuLYSValTYrGlnMetLeuGlnIYST 635
|||||
Db 659 TTGACCATGACTATGAGCAGAGATGAGACTGAGAAAGAGTT---TCCAGATGTCACAAAGT 715
OY 635 rp 635
Db 716 GG 717
RESULT 9
B0317122/c 656 bp mRNA linear EST 17-MAY-2002
LOCUS OVO-CT0387-180300-167-a01 CT0387 Homo sapiens cDNA, mRNA sequence.
DEFINITION B0317122
VERSION B0317122.1 GI:20922891
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 656)
AUTHORS Dias Neto,E., Garcia Corra,R., Verjovsky-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zaio,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
2020263
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV0&L2=QV0-CT03&L=180300-167-a01&L3=2000-03-18&L4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 655.
 Location/Qualifiers
 1. 656
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CT0387"
 /dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site-1: Sma1; Site-2: Sma1; A mini-library was made by cloning products derived from ONESTEP PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 BASE COUNT 152 a 167 c 124 g 213 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2,24e-110 Length: 656
 Score: 1102.00 Matches: 212
 Percent Similarity: 96.80% Conservative: 0
 Best Local Similarity: 96.80% Mismatches: 1
 Query Match: 31.09% Indels: 1
 DB: 14 Gaps: 0

US-09-981-397a-16 (1-671) x BQ317122 (1-656)

107 GUnetSerthrProleuSerValylsGlyArgylleleuGluilleleuGlymet 126
 655 GAGATGACTCTCGGCTTCTGTAAAGAGAGATATTGGAAATCATTTGAGGANTG 596
 127 CysTyrleuHisGlyLysGlyValleuHisLysAspleuLysProGluAsnleuVal 146
 595 TGCTACTTACATGAGAAAGCGCGCATACACAAAGCACTGAACCCGAAATATCTTGT 536
 147 AspAsnAspPheHisIleLysIleAlaAspleuGlyleuAlaSerPheLysMetTrpSer 166
 555 GATATGACTCTCCACATTAAGATCGCACACCTCGGCTTCTTAAAGATGAGGAC 476
 167 LysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAspGlyThrAlaLysLysAsn 186
 475 AAACGTGAATATGAAGACACACATGAGCTGAGGAAAGTGAAGCGCACCGCTAAGAAAT 416
 187 GlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAlaLysProThr 206
 415 GGGCGACCTCTACTACTGAGCGCCGACGCACTGAATGAGTCAACGCAAAAGCCCA 356
 207 GluLysSerAspValTyrSerPheAlaValleuThrPalaIlePheAlaAsnLysGlu 226
 355 GAGAAAGTCGATGTGTACAGCTTCTGTAGTACTCTGGCGCATTTTGCAGAAATAGAGAG 296
 227 ProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCysIleLysSerGlyAsnArg 246
 295 CCATATGAAATATGCTATCTGTGAGCAGCACTGATTAATGCTAATAATCTGGCAACAG 236
 247 ProAspValAspAspIleThrGluTyrCysProArgGluIleIleSerLeuMetLysLeu 266
 235 CCAGATGAGATGATCATGATGAGTCCCAAGAGAAATATATCATGCTCATGAGAGCTC 176
 267 CysTrpGluAlaAsnProGluAlaArgProThrPheProGlyIleGluGluLysPheArg 286
 175 TGCTGGAGAGGAATCCGGAAGCTGGCGCATTTCTGCGATTTGAAGAAATTTTGAAG 116
 287 ProPheTyrLeuSerGluLeuGluGluSerValGluGluLysValLysSerLeuLysLys 306

DB 115 CTTTTTACTTAAAGCATTTGAAAGAAAGTGTACAGAGGACGCGAAGAGTTTAAAGA 56
 QY 306 sCltuTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeuGlnLeuAsp 324
 DB 55 ACAGTATTCACAAAGCAAAATGCGAGTTGTGAAGAGAGAGAGTCTCTTCAACTTGAT 1

RESULT 10
 LOCUS B0647524
 DEFINITION B0647524 960 bp mRNA linear EST 15-JUL-2002
 ACCESSION AGENCOUPT_8352671 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6285126
 VERSION B0647524
 KEYWORDS 5', mRNA sequence.
 SOURCE B0647524.1 GI:21771696
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgs.nci.nih.gov/>
 1 (bases 1 to 960)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LRCM2483 row: n column: 07
 High quality sequence stop: 711.
 Location/Qualifiers
 1. 960
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="6285126"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site-1: Xho1; Site-2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: GCGACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

FEATURES
 source

BASE COUNT 281 a 231 c 236 g 210 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.92e-102 Length: 960
 Score: 1028.00 Matches: 192
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 29.00% Indels: 0
 DB: 14 Gaps: 0

US-09-981-397a-16 (1-671) x B0647524 (1-960)

480 AspProGlyThrAlaGlyProArgValTrrpYArgProIleProSerHisMetProSer 499
 14 GATCCAGACACGACGAGTCCAGAGATTGTGAACAGCCCAATCCAAATCATATGCTAGT 73
 500 leuHisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPhe 519
 74 CTGCTATATATCCAGTGGCTGTAGACCAACTATCTAGGAAATATACACCAATGCAATTC 133
 520 SerSerLeuProProThrAspIleSerIleLysTyrThrIleTyrAsnSerThrGlyLe 539

Db 134 AGCTCCCTGGCCACCAAGATGATCTATAAATATACCATATACATAGTACGCATT 193
QY 540 GlnllleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSer 559
Db 194 CAGATTGGACCTTCAATTTATATGAGATGGTGGCGAGCTTCACTACTACTAGACAGC 253
QY 560 ThrAsnThrAsnPhelysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThr 579
Db 254 ACAAAATCGAACTTCAAGAAGAGCCAGCTGCTAAGTACCAAGCTACTTTGATTAATACC 313
QY 580 ThrSerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTyrLys 599
Db 314 ACTAGTGTGACGATTAACACCTGGACCAATCAGGAAATCTGGGAAAGCATGGGAAA 373
QY 600 AsnCysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyr 619
Db 374 AACTGTGCCCGTAACTGGGCTTACACAGCTCTCAGATTGATGAATTGACCATGACTAT 433
QY 620 GluArgAspLysLeuLysGlyLysValTyrGlnMetLeuGlnLysTyrValMetArgGlu 639
Db 434 GAGCGAGATGAGACTGAAAGAAAGGTTTACCAGATGCTCCAAAAGTGGTGATGAGGAA 493
QY 640 GlyIleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgTle 659
Db 494 GGCATTAAGGAGACCGAGTGGGGAACCTGGCCAGCGCTCCACAGTGTTCAGAGATC 553
QY 660 AspleuLeuSerSerLeuIleTyrValSerGlnAsn 671
Db 554 GACCTTCTGAGACAGCTTGATTTCGTGACCGACAGAC 589

RESULT 11
LOCUS B1663126 775 bp mRNA linear EST 12-SEP-2001
DEFINITION 603286738F1 NCL_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5320856 5',
mRNA sequence.
ACCESSION B1663126
VERSION B1663126.1 GI:15577359
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 775)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-femail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM1813 row: 1 column: 09
High quality sequence stop: 769.
Location/Qualifiers

FEATURES

source
1..775
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5320856"
/clone_1lb="NCL_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI. Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 250 a 156 c 205 g 164 t
ORIGIN
Alignment Scores:
Pred. NO.: 3.52e-101 Length: 775
Score: 1019.50 Matches: 190
Percent Similarity: 85.71% Conservative: 26
Best Local Similarity: 75.40% Mismatches: 35
Query Match: 28.76% Indels: 1
DB: 13 Gaps: 1

US-09-981-397a-16 (1-671) x B1663126 (1-775)

QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGluSer 20
Db 19 ATGCAACACAGACATGCTCTTGAGCAATTTATAGATGCATCCAGTACCTGCTGGAGAG 78
QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyCysPheHisArgThrGlnGly 40
Db 79 ACAGACCTTAGACAGCGGAGCTTCGGAGAGGTGCTTGTTGTTACACAGAGCCATGGA 138
QY 41 LeuMetLleMetLysThrValTyrLysGlyProAsnGlyIleGluHisAsnGluAlaLeu 60
Db 139 TTGTCTATCCTGAAAAAGATATACACAGGCGCCACCGCTGATGATGAGTTCTC 198
QY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValIleLysLeuGly 80
Db 199 TTGGAAGAGGGAAGATGATGACACAGCTGAGACACAGTGGAGTGAACCTACTGGCC 258
QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
Db 259 ATCATCATAGAGAGAGGAGGACTATTCCTGCTGATGAGTACATGAGAGAGGCAACCTG 318
QY 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
Db 319 ATGCACGTGCTAAAGACCCAGATGATGTCCTCCACTTTCATTTGAAGAGAGATATCTGTG 378
QY 121 GluIleIleGluGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
Db 379 GAGGCCATAGAGGAGCATGCTGCTACTTACATGACAAAGTGTGATACCAAGACCTGAAG 438
QY 141 ProGluAsnIleLeuValAspAsnAspPheHisLleLysIleAlaAspLeuGlyLeuAla 160
Db 439 CCTGAGAAATATCCCTGTTGATCGTCACTTTCACATTAAGATAGCCGATTTGGTGCT 498
QY 161 SerPheLysMetTyrPserLysLeuAsnGluGluHisAsnGluLeuArgGluValAsp 180
Db 499 TCCTTTTAAGACATGACCAAACTGACTAAGAGAAACAACAAGAGAGAGTACG 558
QY 181 GlyThrAlaLysLys--AsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsn 199
Db 559 AGCACCCCTAAGAGAGCAATGTTGGTGAACCTTTACTACATGCGACCCGAAACCTTAAT 618
QY 200 AspValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValIleuTyrP 219
Db 619 GACATCAATGCAAAAGCCCGAGAGAGTGGAGAGCTTGACATTTGGCATTTGCTTTGG 678
QY 220 AlaIlePheAlaAsnLysGluProTyrGluAsnAlaIleLysGluGlnGlnIleMet 239
Db 679 GCAATATATTTGCCAAAAAGAGCCCTATGAGAAATCTCATGCTAGCAGCTTGATC 738
QY 240 CysIleLysSerGlyAsnArgProAspValAspAsp 251
Db 739 TGCAATTAATCTGTGGAAACAGGCCCAATGTAGAGGA 774

RESULT 12
LOCUS B1559218 805 bp mRNA linear EST 05-SEP-2001
DEFINITION 603240839F1 NCL_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5294000 5',
mRNA sequence.
ACCESSION B1559218
VERSION B1559218.1 GI:15446532
KEYWORDS EST.

SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 805)
AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rsrab@ncl.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M1743 row: m column: 09
High quality sequence start: 4
High quality sequence stop: 775.

FEATURES
source
Location/Qualifiers
1..805
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5294000"
/clone_lib="NCI CGAP Mand"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
BASE COUNT
246 a 175 c 205 g 179 t
ORIGIN

Alignment Scores:
Pred. No.: 9.42e-97 Length: 805
Score: 979.50 Matches: 198
Percent Similarity: 82.48% Conservative: 28
Best Local Similarity: 72.26% Mismatches: 39
Query Match: 27.63% Indels: 9
DB: 13 Gaps: 2

US-09-981-397A-16 (1-671) x B1559218 (1-805)

QY 96 glutysgluasnleumethisvalleuysalaglumetserthrproleuservallys 115
Db 1 CAGAAAGGCAACCGATGACAGTGTCTTAAGACCCAGATAGATGTGCCCTTTCATTGAAA 60
QY 116 GLYATGILELLEUGLUILLLEIGLUYMETCYSTRYLEUHSGLYLYSGLIYVALLE 135
Db 61 GGAAGGATATCGTGAGGCCATAGAGGCATGTGCTACTACATGACAAAGGTGTGATA 120
QY 136 Hislyaspleuysprogluasnlleuvalaspsnaspphehisillelysila 155
Db 121 CACAAAGGACCTGAGACCTGAGAAATATCTCTGTGATCTGACTTTCACATTAAATACCC 180
QY 156 Aspleuuglyleualaserphelylemetrserlyseuasnasnglulhisasnlu 175
Db 181 GATCTGTGGTGTCTTCTTTAAGACATGAGCAAACTAGACTAAGAGAAAGACACACAG 240
QY 176 leuargluvalasp-glythratalyslys--asnlyglythrleuutyrrymetal 194
Db 241 CAGAAAGAGCTGAGACAGACCTAGAGAACAAATGTGTGTAACCTTACTACTAGTGC 300
QY 194 aProgluHisleuasnspvalasnAlaLysProthgluLysSeraspvalItyrserph 214
Db 301 ACCCGAACCTGTAATGACATCAATGCAAAAGCCACGAGAGAGTGGACGTGTACAGCTT 360

QY 214 eAlavAlValleuTrpAlailepheaAlaasnLysgluProtyrgruAsnAlaileCysG1 234
Db 361 TGCCATTGTCTTCTTGGGCAATATTTGGCAAAAAGAGCCCTTATGATGATGATCTGTAC 420
QY 234 uGlnGlnleuilemetCysIleLysSerGlyAsnArpProaspValaspaIlethG1 254
Db 421 TGAGCAGTTCGTCGATCTGCATATAATCTGGGACAGGCCAAATGTAGAGAAATCCTTGA 480
QY 254 uTYrCysProarpgluilleleserleuemetLysleucysrrpAlaAsnProgluAl 274
Db 481 GTACTGTCCAAGGAGATCATGAGCTCATGTGAGCGGTGCGAGGATCCAGAAGA 540
QY 274 aArgProthrPheProgluIleGluLysPheArpProthyrrleuSerGlnleuG1 294
Db 541 CAGCGACACATTTCTTGGCATTGAAGAAGATTTAGCCCTTTTACTTAAGTCATTTTGA 600
QY 294 uGluSerValGluGluAspVal--LysSerleuysLysGluYrSerAsnGluAsnAla 313
Db 601 AGAATATGTAGAAAGAGATGTGGCAAGTTGACCAAGAAAGATATCCAGATCAAGCCCA 660
QY 314 ValValLysArgmetGlnSerleuGlnleu-AspCysValAlaValProSerSer-Arg 333
Db 661 GTGCTGCAGAGAAATGTTTGCACCTGACACATGACTGTGTACCTTACCTCCAGACAGGT 720
QY 333 eAsnSerAlaThrcGluGlnProgluSerleuHisSerSerGlnlyleuGlymetGlyP 353
Db 721 CAAATTTA-----GAAACACCTGATCGATCGTCACAGCTCCAGGGGCTCCAGATGGTCT 774
QY 353 roval-GluGluSerTrpPheAlaProSer 362
Db 775 CTGTGGAGAGATCGGGTACTTCTTCC 804

RESULT 13
B6691740
LOCUS
DEFINITION
B6691740
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 649)
AUTHORS
Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
TITLE
Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@nrl.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -m1nscore 18
and -minmatch 12 options.
PCR primers
FORWARD: AGCAACAGCATATGACCAT
BACKWARD: GTTTCACGATCAGCAGC
Plate: 99 row: P column: 22
Seq primer: ATTAGGTGACATATG.
FEATURES
source
Location/Qualifiers
1..649
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;

Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

BASE COUNT 173 a 162 c 193 g 121 t

ALIGNMENT SCORES:

Pred. No.: 2,066-86 Length: 649
Score: 884.00 Matches: 162
Percent Similarity: 89.52% Conservative: 26
Best Local Similarity: 77.14% Mismatches: 22
Query Match: 24,948 Indels: 0
Gaps: 0

US-09-981-397a-16 (1-671) x BG691740 (1-649)

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DB 19 GTGCTCAAGAGCCCGGTCAGCATCCCTGTCGCGAAGGAGGATCATATGAGAGC 78
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DB 79 ATCGAAGAAATCGCTTACCTCCAGGAGAGGGGTGATACACAGGACCTCAAGCCAGAA 138
OY 143 AsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPhe 162
DB 139 AATATCCCTGTTGACAGGAGCTTCCACATCAAGATGAGCTGGGGTCTCTTC 198
OY 163 LysMetTrpSerLysLeuAsnAsnGluHisAsnGluLeuArgGluValAspGlyThr 182
DB 199 AAGACGTGAGCAGCATGACGAGAGGAGACACATGAGCAGGAGCGGCGGAGT 258
OY 183 AlaLysLysAsnGlyLysThrLeuTyrMetAlaProGluHisLeuAsnAspValAsn 202
DB 259 GCCGGGAAGAGCGGTGGACGCTGACATGAGCCCTGAGACCTTACAGATGTAC 318
OY 203 AlaLysProThrGluLysSerAspValTyrSerPheAlaValLeuTrpAlaIlePhe 222
DB 319 TCCAGGCCCTCCGAGAAGTCCGAGCTTTCAGCTTTCGACATGCTCTGGGCGATCTTC 378
OY 223 AlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGlnLeuIleMetCysLys 242
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OY 243 SerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIleLeuSer 262
DB 439 TCTGGGAAGAGCCAGAGCTGAGGACATCTTGAAGTCTCCCGGGAGATTATGAC 498
OY 263 LeuMetLysLeuCysTyrPgluAlaAsnProGluAlaArgProThrPheProGlyTyrIleGlu 282
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LOCUS M80-NT0039-010500-002-c01 NT0039 Homo sapiens CDNA, mRNA sequence.
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ACCESSION AM890282.1 GI:8054487
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 563)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,

TITLE
JOURNAL
MEDLINE
COMMENT

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=st2-M80-NT0039-010
500-002-c01&t3=2000-05-01&t4=1)
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High quality sequence stop: 466.
Location/Qualifiers

FEATURES

1..563
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/db_xref="taxon:9606"
/clone_lib="NT0039"
/dev_stage="Adult"
/note="Organ: nervous tumor; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 115 a 131 c 140 g 177 t

ORIGIN

Alignment Scores:
Pred. No.: 5,66-85 Length: 563
Score: 870.00 Matches: 165
Percent Similarity: 94.38% Conservative: 3
Best Local Similarity: 92.70% Mismatches: 9
Query Match: 24,548 Indels: 1
Gaps: 0

US-09-981-397a-16 (1-671) x AM890282 (1-563)

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OY 410 GluArgArgArgValSerHisAspPheAlaGlnGlnArgProTyrGluAsnPhe 429
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OY 430 GlnAsnThrGluGlyLysGlyThrValTyrSerSerAlaAlaSerHisGlyAsnAlaVal 449
DB 442 CAGATACAGAGGGAAGAGCAGCTGATTCAGAGTGAGCCAGATGATGATGAGAGTGC 383
OY 450 HisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyr 469
DB 382 CACGAGCCCTCAGGCTCAGCAGCAACCTCAAGTACTATCAGAACATGATTTATAT 323
OY 470 SerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaGlyProArgValTyr 489
DB 322 AGCTCACATGACTTTGGACAGACACCTGATCCAGAGAGAGGTTCCAGAGTGG 263
OY 490 TyrArgProLeuProSerHisMetProSerLeuHisAsnIleProValProGluThrAsn 509
DB 262 TACAGGCCAATTCACAGTCAATATGCTGATATATATCCAGTGCCTGAGACCAAC 203

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 25, 2003, 20:39:11 ; Search time 100 Seconds
(Without alignments)
2057.801 Million cell updates/sec

Title: US-09-981-397A-16
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3545	100.0	2617	1	US-09-161-443-1 Sequence 1, Appl
3	3529	99.5	2137	1	US-08-444-005-16 Sequence 16, Appl
4	3505	98.9	9687	4	US-09-133-944-2 Sequence 2, Appl
5	3505	98.9	9687	4	US-09-208-827-2 Sequence 2, Appl
6	2423.5	68.4	2268	4	US-08-444-005-14 Sequence 14, Appl
7	521	14.7	606	4	US-09-328-111-495 Sequence 495, Appl
8	448	12.6	1873	3	US-09-329-418-1 Sequence 1, Appl
9	448	12.6	1873	4	US-09-531-914-1 Sequence 1, Appl
10	446	12.6	1537	3	US-09-329-418-2 Sequence 2, Appl
11	446	12.6	1537	4	US-09-531-914-2 Sequence 2, Appl
12	410.5	11.6	3516	3	US-09-188-930-257 Sequence 257, App

13	375.5	10.6	1888	3	US-09-188-930-66 Sequence 66, Appl
14	371	10.5	1620	4	US-09-099-041A-3 Sequence 3, Appl
15	371	10.5	1620	4	US-09-245-281-3 Sequence 3, Appl
16	371	10.5	1620	4	US-09-207-359B-3 Sequence 3, Appl
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20	371	10.5	1931	4	US-09-470-271-2 Sequence 2, Appl
21	371	10.5	1931	4	US-09-207-359B-3 Sequence 1, Appl
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23	371	10.5	2502	4	US-09-069-023-2 Sequence 2, Appl
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28	354.5	10.0	4989	3	US-08-746-559A-1 Sequence 1, Appl
29	354.5	10.0	4989	4	US-08-880-313A-9 Sequence 9, Appl
30	354.5	10.0	4989	4	US-09-199-926-3 Sequence 3, Appl
31	354.5	10.0	4989	4	US-08-864-641B-17 Sequence 17, Appl
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37	337.5	9.5	1521	2	US-08-604-989A-10 Sequence 10, Appl
38	337.5	9.5	1713	4	US-09-741-154-1 Sequence 1, Appl
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44	319.5	9.0	1788	4	US-09-529-279-14 Sequence 14, Appl
45	319.5	9.0	2656	2	US-08-685-625A-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-132-118-1
; Sequence 1, Application US/09132118
; Patent No. 6211337
; GENERAL INFORMATION:
; APPLICANT: BAICHUWAL, VIJAY R
; APPLICANT: HUANG, JIANING
; APPLICANT: HSU, HAILING
; APPLICANT: GOEDEL, DAVID V
; TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/132.118
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: 795-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342

:- INFORMATION FOR SEQ ID NO: 1:
:- SEQUENCE CHARACTERISTICS:
:- LENGTH: 2016 base pairs
:- TYPE: nucleic acid
:- STRANDEDNESS: double
:- TOPOLOGY: linear
:- MOLECULE TYPE: cDNA
:- FEATURE:
:- NAME/KEY: CDS
:- LOCATION: 1..2013
US-09-132-118-1

Alignment Scores:
Pred. No.: 0 Length: 2016
Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-981-397a-16 (1-671) x US-09-132-118-1 (1-2016)
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DB 121 CTCATGATCAGAAACAGTGTACAGAGGCCCAACTCATTTGACACACAGAGCCCTC 180
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QY 381 GluAlaAsnTyrHisLysLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
DB 1141 GAAGCCACTACCATCTTTATGCGACGCGCATGAGACAGCAGAGAAACAGCAGCCACAGA 1200
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QY 421 AlaGlnGlnArgProTyrGluAsnPheGluAsnThrGluGlyLysGlyThrValTyrSer 440
DB 1261 GCACAGCAAGACCTTTACAGAAATTTTCAGATTCAGAGGGGAAAGGCACCTGTTATTC 1320
QY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
DB 1321 AGTCGAGCAGTCAATGGAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1380
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QY 521 SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
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QY 541 IleGlyAlaTyrAsnTyrMetGluIleGlyGlyHisSerSerLeuLeuAspSerThr 560
DB 1621 ATTGGAGCTTAAATTAATGAGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1680
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QY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
Db 1981 CTCTGAGCAGCTTGATTTAGTCAAGCCAGAAC 2013

RESULT 2
US-09-161-443-1
: Sequence 1, Application US/09161443A
: Patent No. 6020198
: GENERAL INFORMATION:
: APPLICANT: C. Frank Bennett
: APPLICANT: Lex M. Cowsett
: TITLE OF INVENTION: ANTISENSE MODULATION OF RIP-1 EXPRESSION
: FILE REFERENCE: RFS-0011
: CURRENT APPLICATION NUMBER: US/09/161.443A
: CURRENT FILING DATE: 1998-09-25
: NUMBER OF SEQ ID NOS: 47
: SEQ ID NO 1
: LENGTH: 2617
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(2016)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 2141
: OTHER INFORMATION: unknown
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: NAME/KEY: unsure
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: OTHER INFORMATION: unknown
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: OTHER INFORMATION: unknown
US-09-161-443-1

Alignment Scores:
Pred. No.: 0 Length: 2617
Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-981-397a-16 (1-671) x US-09-161-443-1 (1-2617)

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Db 121 CTCATGATCATGAAGAAACAGTGTACAGAGGCCCCAACTCATTTGAGCACACAGAGCCCTC 180
QY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValIleLysLeuLeuGly 80
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Db 181 TTGAGAGAGCCCAACAGATGATGAACAGACTGAGACACAGCCGGGTGGTGAACCTCTCGGGC 240
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QY 141 ProGluAsnIleLeuValAspAsnSerPheHisIleLysIleAlaAspLeuGlyLeuAla 160
Db 421 CCTGAAATATCTGTTGATTAATGACTTCCACATTAAATGATGCGAGACCTCGGCTTCC 480
QY 161 SerPheLysMetTrpSerLysLeuAsnGlnGluHisAsnGluLeuArgGluValAsp 180
Db 481 TCCTTTAGATGTGAGCAACTGATATATGAGGCAACATGACTGAGGGAAGTGGAC 540
QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAsp 200
Db 541 GGCACCCCTAAGAAAGATGGCGGCACCTTACTACTACATGCGCCGACACCTGAATGAC 600
QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValIleuTrpAla 220
Db 601 GTCAAGGCAAGCCCAACAGAGAGATGGATGTACACTTGGCTGTAGTCTCGGGCG 660
QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGluLeuIleMetLys 240
Db 661 ATATTGGCAATTAAGAGACCATATGAATGCTATCTGTGACACACACTTGATATGTGC 720
QY 241 IleLysSerGlyAsnArgProAspValAspIleIleThrGluTyrCysProArgGluIle 260
Db 721 ATAAATCTGGGAAGAGCCAGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 261 IleSerLeuMetLysLeuGlyTrpGluAlaAsnProGluAlaArgProThrPheProGly 280
Db 781 ATCAGTCTCATGAGACTGTGCTGGGAGACGATCCGGAAGCTGGCGCACATTTCTCGGC 840
QY 281 IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluLysSerValGluLysAsp 300
Db 841 ATTGAAGAAAATTTAGGCTTTTATTAACTCAATTAGAAAGAAAGCTGTACAGAGAC 900
QY 301 ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValIleLysArgMetGlnSer 320
Db 901 GTGAAGAGTTTAAAGAAAGAGATTCACAACGAAATGCAATGTCAGAGATGCAATGCAATGCT 960
QY 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
Db 961 CTTCAACTGTGATGTGTGGAGTACCTTCAAGCCGCTGAATTCAGCCACAGAAACAGCCT 1020
QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla 360
Db 1021 GGTTCACGTCCACAGTTCACAGGACTTGGGATGGCTCTGTGGAGAGATCTCTGTTTCT 1080
QY 361 ProSerLeuGlnHisProGlnGluLysGlnProSerLeuGlnSerLysLeuGlnAsp 380
Db 1081 CCTTCCTCGAGAGACCCACAGAGAGAGATGAGCCACCTGACAGAGATAAATCCCAAC 1140
QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
Db 1141 GAAGCAACTACCACTTTATGCGACCGCATGCGACAGAGAGCAACACACAGCCACGA 1200
QY 401 GlnAsnValAlaTyrAsnArgGluGluGluTyrArgArgValSerHisAspProPhe 420
Db 1201 CAGATATGCGCTTACACAG 1260
QY 421 AlaGlnGluArgProTyrGluAsnProPheGlnAsnThrGluGlyLysGlyThrValTyrSer 440
Db 1261 GCACAGCAAGACCTTACAGAAATTTTCAGATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
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OY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
DB 1321 AGTCAGCGCAGTCAGTATGATGCACTGCACCGCCCTCAGGCTCACCAGCCACTCA 1380
OY 461 ValLeuTyrglnAsnAsnGlyLeuTyrsSerHisGlyPheGlyThrArgProLeuAsp 480
DB 1381 GTACTGTATCAGAACAAATGGATTATATAGCTCATGCTTGTGGAACAAGCACTGGAT 1440
OY 481 ProGlyThrAlaGlyProArgValTrpIlyrArgProIleProSerHisMetProSerLeu 500
DB 1441 CCAGAACACGACGATCCCAAGATTGGTACAGGCGCAATCCAGTCATATGCTAGTCTG 1500
OY 501 HisAsnIleProValProGluThrAsnTyrlleuGlyAsnThrProThrMetProPheSer 520
DB 1501 CATATATCCAGTCTCTGAGACCAACTATCTAGAAATATACCCACCATGCTATCAGC 1560
OY 521 SerLeuProProThrAspGluSerIleIyTyThrIleIyAsnSerThrGlyIleGln 540
DB 1561 TCCTTGCCACCAACAGATGAATCTATAAATATACCAATATCAATAGTACTGGCATTCAG 1620
OY 541 IleGlyAlaTyraAsnTyrlMetGluIleGlyGlyThrSerSerLeuLeuAspSerThr 560
DB 1621 ATTGAGACCTACAAATTATATGAGATGTGTGGAGAGTCTCATCTACTACACAGACA 1680
OY 561 AsnThrAsnPhelysGluGluProAlaAlaIyTyrglnAlaIlePheAspAsnThrThr 580
DB 1681 AATACGACTTCAAGAAGAGAGCCAGCTGCTAGTACCAAGCTATCTTGATATATCCACT 1740
OY 581 SerLeuThrAspIlyHisLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsn 600
DB 1741 AGTCAGCGATAAACACCTGACCCCAATCAAGGAAATCTGGGAACACACGGAAGAAAC 1800
OY 601 CysAlaAlaGlyLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTrpGlu 620
DB 1801 TGTGCCCTTAACCTGGCTTACACAGATCTCAGATTGATGAATTGACCATGACTATATGAG 1860
OY 621 ArgAspGlyLeuLysGlyLysValTyrglnMetLeuGlnIyStrpValMetArgGlyGlu 640
DB 1861 CGAGATGAGCTGAAGAAAGATTACCAAGATGCTCCAAAGATGGGTGATGAGGGAAGGC 1920
OY 641 IleIyGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
DB 1921 ATAAAGGAGCGACCGTGGGGAAGCTGGCCAGCGCTCCACACAGTGTCCAGAGATCGAC 1980
OY 661 LeuLeuSerSerLeuIleTyValSerGlnAsn 671
DB 1981 CTTCGAGCAGCTTATTTAGCTACGCCAGAAC 2013

```

RESULT 3

US-08-444-005-16

Sequence 16, Application US/08444005

Patent No. 5674734

GENERAL INFORMATION:

APPLICANT: Leder, Philip

APPLICANT: Seed, Brian

APPLICANT: Stanger, Ben Z.

APPLICANT: Lee, Tae-Ho

APPLICANT: Kim, Emily

TITLE OF INVENTION: CELL DEATH PROTEIN

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street, Suite 3100

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,005
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00383/026001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-444-005-16

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Alignment Scores:
Pred. No.: 0 Length: 2137
Score: 3529.00 Matches: 668
Percent Similarity: 99.70% Conservative: 1
Best Local Similarity: 99.55% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 1 Gaps: 0

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US-09-981-397A-16 (1-671) x US-08-444-005-16 (1-2137)

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OY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
DB 1 ATGCACACGACATGCTCTTGATGTCATTAAGATGAATCCAGTACTTCTTGAGAGCT 60
OY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyCysPheHisArgThrGlnGly 40
DB 61 GCAGAACTGGACAGCGCGAGGCTTCGGAAGCTGTCTGTGTTCACACAGAACCCAGGGA 120
OY 41 LeuMetIleMetLysThrValTyrlTyrglyProAsnGlyIleGlnHisAsnGluAlaLeu 60
DB 121 CTCATGATCATGAAGAAAGTGTACAAAGGGCCCACTCATTTGAGACACAGAGGCCCTC 180
OY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValIValLysLeuGly 80
DB 181 TTGAGAGGAGCGGAAGATGATGACAGACTGAGACACACCCGGTGTAAACTCTCTGGGC 240
OY 81 ValIleIleGluGluGlyLysTyrsSerLeuValMetGluTyrlMetGluLysGlyAsnLeu 100
DB 241 GTCATCATGAGAGGAGGAGAGTACTCCCTGCTGATGAGATGACATGAGAGGCAACCTG 300
OY 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
DB 301 ATGCACGTGCTGAAGCCGAGATGACTCCGCTTCTGTGTAAGAGGAAGATTAATTTTG 360
OY 121 GluIleIleGluGluMetCysTyrlLeuHisGlyValIleHisLysAspLeuLys 140
DB 361 GAATCATTTGAAGGAATGCTACTTACATGGAAGGCGGATACACAAAGACTGAGAG 420
OY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB 421 CCTGAATATTCCTTGTGATATGACATTCACATTAAGATGACGACACTCGGCTTGCC 480
OY 161 SerPheLysMetLysPheSerLysLeuAsnAsnGluGlnHisAsnGluLeuArgGluValAsp 180
DB 481 TCCTTTAAGATGTGAGCAAACTGAATATATGAAGGCACAATGAGCTGAGGGAAGTGGAC 540
OY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrlTyrlMetAlaProGluHisLeuAsnAsp 200
DB 541 GGACACGCTAGAGAAATGGCGGACCTCTACTACATAGGGCCGAGACACTGAAATGAC 600
OY 201 ValAsnAlaLysProThrGluLysSerAspValTyrlSerPheAlaValIleLeuTrpAla 220

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Db      601  GTCAAGCAAGCCACAGAGAGAGTGGAGTGTACAGCTTTGCTGTAGTACTCTGGCG 660
Qy      221  ILePheAaAnLysGluProTyrGluAsnAlaIleCysGluGlnGlnIleMetCys 240
      |||
Db      661  ATATTGGCAATATAGAGGCCATATGAAATCTATCTGTGACGACGACTTGTATATGTC 720
Qy      241  ILeLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
      |||
Db      721  ATAAATCTGGGAGACAGGCCAGATGTGGATGACATCATGTGACTGCTGCCCAAGAAATT 780
Qy      261  ILeSerLeuMetLysLeuGlyTyrGluAlaAsnProGluAlaArgProThrPheProGly 280
      |||
Db      781  ATCAAGTCTCATGAAGCTCTGCTGGGAACCGAATCCGGAAGCTCGGCCACATTTCTGGC 840
Qy      281  ILeGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluLysAsp 300
      |||
Db      841  ATTGAAGAAATTTAGGCTTTTATTTATTTAGTCATTAGAGAAAGAGTGAAGAGAGAC 900
Qy      301  ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValLysArgMetGlnSer 320
      |||
Db      901  GTGAAGAGATTAAAGAAAGAGTATTCAAACGAAATGCAAGTGTGAGAGAGATGCACT 960
Qy      321  LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluLysPro 340
      |||
Db      961  CTTCAACTGATGTGTGGCAGTCTTCAAGCGGTCAAATTCAGCCACAGAAAGAGCT 1020
Qy      341  GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTyrPheAla 360
      |||
Db      1021  GGTTCACCTGCACACTTCCACAGGACTTGGATGGGTCTGTGGAGAGATCCTGGTTTGGT 1080
Qy      361  ProSerLeuGlnHisProGlnGluAsnGluProSerLeuGlnSerLysLeuGlnAsp 380
      |||
Db      1081  CCTTCCTCGAGCAGCCACAGAGAGAGATGAGCCACCTGCAAGATGAATCACTCCAAAC 1140
Qy      381  GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
      |||
Db      1141  GAAGCCCAACTACCACTTTATGTGACCGCGGTGACAGCAGAGCAAGAAACACAGCCCA 1200
Qy      401  GlnAsnValAlaTyrAsnArgGluGluLysArgArgArgValSerHisAspProPhe 420
      |||
Db      1201  CAGAAATGGCTTTCACACAGAGAGAGAGAAAGAGAGCCAGGGTCTCCCATGACCTTTT 1260
Qy      421  AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer 440
      |||
Db      1261  GCACAGCAAGAGCCTTACGAGAAATTTTCAGAAATACAGAGGAGGAAAGGACATGTTAT 1320
Qy      441  SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
      |||
Db      1321  AGTCACCCAGCTCATGTGTAATGACAGTCACAGCCATCCAGGCTCACCAGCCAACTCAA 1380
Qy      461  ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
      |||
Db      1381  GTACTGTATCAGAACATGATGATTTATATGCTCACATGGCTTTGGAAACAGACCACTGGAT 1440
Qy      481  ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
      |||
Db      1441  CCAGAGAACAGAGAGCTCCAGAGTTTGGTACAGGCCAATTCACAGTCATATGCCAAGTCTG 1500
Qy      501  HisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSer 520
      |||
Db      1501  CATATATATCCAGAGCTCGAGACCACTATCTAGGAAATTTCTCCACCATCCATTCAAGC 1560
Qy      521  SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
      |||
Db      1561  TCCCTGGCACCAAGATGATCTATATAATATATACCATATACATATGACTGGGCTTCAG 1620
Qy      541  IleGlyAlaTyrAsnTyrMetGluIleGlyLysThrSerSerSerLeuLeuAspSerThr 560
      |||
Db      1621  ATTGAGACCTTACATATATATGATGATGTGGTGGACGAGTTCAATCAGTACTAGACAGACA 1680
Qy      561  AsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
      |||
Db      1681  AATACGAACCTTCAAGAGAGAGCCAGCTGCTAAGTACCAAGCTATCTTGTATATACCACT 1740

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Qy      581  SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTyrLysAsn 600
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Db      1741  AGTCGACGAGATTAACACCTGACCCATTCAGGAAATCTGGCAACACCTCGCAAAAC 1800
Qy      601  CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu 620
      |||
Db      1801  TGTGCCCTTAACCTGGCGCTTCACACAGTCTCAGATGTGAAATTCAGCATGACTATGAG 1860
Qy      621  ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrPValMetArgGluGly 640
      |||
Db      1861  CGAGATGACCTGAAAGAAAGCTTTTACCATGCTCCAAAAGTGGTGTATGAGGAAAGGC 1920
Qy      641  IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
      |||
Db      1921  ATAAAGAGGACGACGCTGGGAGAGCTGGCCACAGCGCTCCACAGCTGTCCAGATGAGAC 1980
Qy      661  LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
      |||
Db      1981  CTTCTGACGACCTTGATTTACGTACAGCCAGAAC 2013

RESULT 4
US-09-133-944-2
: Sequence 2, Application US/09133944
: Patent No. 6280937
: GENERAL INFORMATION:
: APPLICANT: Luo, Ying
: APPLICANT: Yu, Pei Wen
: APPLICANT: Lorens, James
: TITLE OF INVENTION: SHUTTLE VECTORS
: FILE REFERENCE: A66252/DJB/DAV
: CURRENT APPLICATION NUMBER: US/09/133, 944
: CURRENT FILING DATE: 1999-08-14
: EARLIER APPLICATION NUMBER: 09/133, 949
: EARLIER FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 9687
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: constructed
: US-09-133-944-2

Alignment Scores:
Pred. No.: 0 Length: 9687
Score: 3505.00 Matches: 668
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 2
Query Match: 98.87% Indels: 1
DB: 4 Gaps: 0

US-09-981-397A-16 (1-671) x US-09-133-944-2 (1-9687)
Qy      2  GlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGluSerAla 21
      |||
Db      1134  CAACCAAGACATGCTCTTGAATGTCAATTAAGTAAATTCACATGACTTCTGGAAGTGA 1193
Qy      22  GluLeuAspSerGlyGlyPheGlyLysValSerLeuCysPheHisArgThrGluGlyLeu 41
      |||
Db      1194  GAATCGACAGCGAGAGGCTTTGGAGAGGTGTCTGTGTCTTCCACAGAACCCAGAGGACTC 1253
Qy      42  MetIleMetLysThrValTyrLysGlyProAsnGlyIleGluHisAsnGluAlaLeuLeu 61
      |||
Db      1254  ATGATTCATGAAGAAAGTGTACAGGGGCCCAACTGCAATTCAGCAACAGAGCCCTCTTG 1313
Qy      62  GluGluAlaLysMetMetAsnArgLeuArgHisSerArgValAlaLysLeuLeuGlyAla 81
      |||
Db      1314  GAGAGGGGGAAGATGATGAACAGACTGAGACACAGCCGGGTGGTGAAGCTTCTGGCGCTC 1373
Qy      82  IleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMet 101

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Db      1374 ATCATAGAGGAGGAGAGTACTCCCTGGATGAGTACATGAGAGGCAACCTGANG 1433
QY      HISValleuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleLeuLeuGlu 121
Db      1434 CAGGTCGTGAAGAGCGAGATGAGTACTCCGCTTCTGTGTAAGAGGATTAATTTGGGAA 1493
QY      112IleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysPro 141
Db      1494 ATCATTTGAAGGAATGTGCTACTTACATGA - AAGAGCTGATATACAGAGACCTGAAGCTT 1552
QY      142 GluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSer 161
Db      1553 GAAATATATCCTTGTGATATATGCTTCCACATTAGATCGCAGACCTCGGCTTCCTCC 1612
QY      162 PheLysMetTyrPsrSerLysLeuAsnAsnGluGluHisAsnGluLeuArgLysValAspGly 181
Db      1613 TTTTAAGATGTGGAGCAAACTGATATATGAGAGCAATGAGCTGAGGAGAGTGAAGCGGC 1672
QY      182 ThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspVal 201
Db      1673 ACCGCTAAGAAGAATGGGGGACCCCTACTACTACATGGCGCCGAGACCTGATGATACGTC 1732
QY      202 AsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuThrPalatle 221
Db      1733 AAGCAAGAGCCCAAGAGAGATCGGATGTGTACAGCTTGTGTGTGTGTGTGTGTGTGTGT 1792
QY      222 PheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCysIle 241
Db      1793 TTTGCAATTAAGAGACCATATGAAATGCTATCTGTGACGACCAATGATTAATGTGCATA 1852
QY      242 LysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgIleIleIle 261
Db      1853 AAATGTGGAGACAGCCAGATGTGATGATGATCATCATGATGATGATGATGATGATGATGAT 1912
QY      262 SerLeuMetLysLeuCysTyrGluAlaAsnProGluAlaArgProThrPheProGlyIle 281
Db      1913 AGTCTCAAGAGCTCTGTGTGGAGACGATCGGAGAGCTCGGCCACATTTCTCTGGCATTT 1972
QY      282 GluGluLysPheArgProPheTyrLeuSerGlnLeuGluLysValGluLysAspVal 301
Db      1973 GAAGAAATTTTAAAGCCTTTTATTTAATGATCAATTAGAGAAAGCTGTGAGAGAGACGTG 2032
QY      302 LysSerLeuLysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeu 321
Db      2033 AAGAGTTTAAAGAAAGATATTCAAAACGAAATGCAAGTTGCAAGAGATGCAAGTCTCTT 2092
QY      322 GlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluInProGly 341
Db      2093 CAAGTGTATGTGTGGAGTACTCTTCAAGCCGCTCAAAATTCAGCCACAGAACAGCCTGCT 2152
QY      342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTyrPheAlaPro 361
Db      2153 TCACGTGCACAGTTCACAGAGCACTTGAGTGGTCTCTGTGGAGAGATCCTGTGTTCTCTCT 2212
QY      362 SerLeuGlnHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGlu 381
Db      2213 TCCTGTGGAGCACCCACAGAGAGATGAGCCACCTGCGAGAGTAACCTCCAAACAGCAA 2272
QY      382 AlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnInProArgGln 401
Db      2273 GCCAAGTACCAATCTTTATGGACGCCGATGAGACAGCAGACGAAACACACACCCGAGAG 2332
QY      402 AsnValAlaTyrAsnArgGluGluLysArgArgArgValSerHisAspProPheAla 421
Db      2333 AATGTGCTTACACACAGAGAGAGAGAAAGACACCCAGAGCTCTCCATGACCTTTTCCA 2392
QY      422 GlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSerSer 441
Db      2393 CAGCAAGAGCCCTTACAGAAATTTTACAGATACAGAGGAGAAAGGACACTGTTATTCAGT 2452
QY      442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal 461

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Db      2453 GCAGCCAGTATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2512
QY      462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
Db      2513 CTGTATCAGAAACAAATGATATATATGATGATGATGATGATGATGATGATGATGATGAT 2572
QY      482 GlyThrAlaGlyProArgValTyrPtyArgProIleProSerHisMetProSerLeuHis 501
Db      2573 GGAACAGCAGGTCCTCCAGATTTGTGTACAGGCCAATTTCCAGTCATATGCTGTGAT 2632
QY      502 AsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSer 521
Db      2633 AATATCCAGTCTGAGACCACTATATGAGAAATATACACCACCATGCTATGAGTCC 2692
QY      522 LeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIle 541
Db      2693 TTGCCACACAGAGATGATCTTAAATATACCAATATCAATATGATGATGATGATGATGAT 2752
QY      542 GlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThrAsn 561
Db      2753 GGAGCCTACATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2812
QY      562 ThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer 581
Db      2813 ACGAATTCAAAGAGAGAGACCATCTCTAAGTACCAAGCATATCTTTGATTAATACCATAGT 2872
QY      582 LeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisIleThrLysAsn 601
Db      2873 CTGACGAGTAAACACCTGACCAATCAAGGAAATCTGGGAAACACCTGGGAAACACCTGT 2932
QY      602 AlaArgLysLeuGluPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGluArg 621
Db      2933 GCCCTTAAACTGTGGCTTCCACAGTCTCAGATTTGATGAAATTTGACCATGATATAGCGA 2992
QY      622 AspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTyrPValMetArgGluGlyIle 641
Db      2993 GATGACCTGAAGAAAGATTTTACAGATGCTCCAAAGTGGTGTATGAGGAGAGCATTA 3052
QY      642 LysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAspLeu 661
Db      3053 AAGGAGCCACCGTGGGAGAGCTGGCCCAAGCGCTCCACAGTGTTCAGGATGACCTT 3112
QY      662 LeuSerSerLeuIleTyrValSerGlnAsn 671
Db      3113 CTGACGACCTGATTTAGCTACGACCAAGAC 3142

RESULT 5
US-09-208-827-2
; Sequence 2, Application US/09208827
; Patent No. 6391582
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHOT/LE VECTORS
; FILE REFERENCE: A66252-1/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/208,827
; CURRENT FILING DATE: 1998-12-09
; EARLIER APPLICATION NUMBER: 09/133,949
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 9687
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: constructed
US-09-208-827-2
Alignment Scores: 0 Length: 9687
Pred. No.:

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Score: 3505.00 Matches: 668
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 2
Query Match: 98.87% Indels: 1
DB: 4 Gaps: 0

US-09-981-397a-16 (1-671) x US-09-208-827-2 (1-9687)

QY 2 GluProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGluSerAla 21
DB 1134 CAACGACACATGCTCTTGAATGATCATTAAGATGAATCACTGACTCTCTGAGAGTGC 1193
QY 22 GluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheIleSarGlyThrGlnGlyLeu 41
DB 1194 GAACCTGACACAGCGAGGCTTTGGAGAGTCTCTGTTGTTCCACAGAACCCAGGAGACTC 1253
QY 42 MetIleMetLysThrValIleTyrLysGlyProAsnGlyIleGlnHisAsnGluAlaLeuLeu 61
DB 1254 ATGATCTCATGAACACAGTGTACAGAGGCCCCCACTGCTATGACACACAGAGGCCCTCTTG 1313
QY 62 GluGlnAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGlyVal 81
DB 1314 GAGAGGCGCAAGATGATGACACAGACGACACAGCGGGTGGTGGAGCTCTGGGGCTC 1373
QY 82 IleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMet 101
DB 1374 ATCATATGAGAGAGGAGGAGTACTCCCTGCTGATGGAGTACATGAGAAAGGCAACCTGATG 1433
QY 102 HisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeuGlu 121
DB 1434 CACCTGCTGAAGCGAGATGATGATCTCCCTTCTGTAAAGAGAGATTAATTTGGCAA 1493
QY 122 IleIleGluGluMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysPro 141
DB 1494 ATCATGAGAGAAATGCTCTACTACTACATGA-AAAGCGGATACACAGAGACTGAAGCT 1552
QY 142 GluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSer 161
DB 1553 GAAATATTCCTTCTGTGAATGACTTCCACATTAAGATCCGACAGCTCGGCGCTTCCCTCC 1612
QY 162 PheLysMetTrpSerLysLeuAsnAsnGluGlnHisAsnGluLeuAsnArgIleValAspGly 181
DB 1613 TTATAGATGTGGACCAACTGAATTAATGAAGACACATGAGTGGAGGAGTGGAGCGC 1672
QY 182 ThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaProGluHisLysAsnAspVal 201
DB 1673 ACCGCTAAGAGATGGCGGACCTCTACTACTAGTGGCGGCGGACACTGAATGACGCTC 1732
QY 202 AsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValIleLeuTrpAlaIle 221
DB 1733 AACGCAAAAGCCACAGAGAGTGGATGTGTACAGCTTTGCTGTAGTACTCTGGGCGATA 1792
QY 222 PheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGlnIleMetCysIle 241
DB 1793 TTATGCAATTAAGAGCGCATTAAGAAATGTATGTGTAGACGACGAGTTGATTAATGTGATA 1852
QY 242 LysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIleIle 261
DB 1853 AAATCTGGGAAGCCAGATGTGATGACATCTCTGAGTACTGCCCAAGAGAAATTAATTC 1912
QY 262 SerLeuMetLysLeuGlyTyrGluAlaAsnProGluAlaArgProThrPheProGlyIle 281
DB 1913 AGTCTCATGAAGCTCTGCTGGAGAGCAATCCGAGACCTCGGCGGACATTTCCGGCATT 1972
QY 282 GluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspVal 301
DB 1973 GAAGAAAAAATTTAGCGCTTTTATTTAATTAAGCAATTAAGAAAGTGAAGAGAGAGAGTGT 2032
QY 302 LysSerLeuLysLysGlyTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeu 321
DB 2033 AAGAGTTTAAAGAAAGATATTCAAAGAAATCACTGTTGGAAGAGAAATGCACTCTCTT 2092
QY 322 GlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnGlnProGly 341

DB 2093 CAACCTGATTTGTGGACAGTACCTTCAAGCCGGTCAAAATTCAGCCACAGAACACCTGTGT 2152
QY 342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaPro 361
DB 2153 TCACTGCACACTTCCACAGGACCTTGGATGGGTCTCTGGAGAGACTCTGTTGTCTCTT 2212
QY 362 SerLeuGlnHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGlu 381
DB 2213 TCCCTGGAGACCCACAAAGAGATGAGCCGACGCTGCAGAGTAAACTCCAAAGACGAA 2272
QY 382 AlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGln 401
DB 2273 GCCAACTACCATCTTTATGCGCAGCCGATGACAGAGGACAGACAAACAGCACCCACAGAC 2332
QY 402 AsnValAlaTyrAsnAspGluGluGluValArgArgArgValSerHisAspProPheAla 421
DB 2333 AATGTGCTTACACAGAGAGAGAGAGAAAGAGAGAGAGGCTCCATGACCTTTTGCA 2392
QY 422 GlnGlnArgProTyrGluAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSerSer 441
DB 2393 CAGCAAGACCTTTCAGAGAAATTTTCAGATATCAGAGGAAAGGACACTGTTATTTCCAGT 2452
QY 442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal 461
DB 2453 GCAGCCAGTCACTGTGTAATGCGATGACACAGCCCTCAGGCGCTCAGCAGCAACTCAAGTA 2512
QY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
DB 2513 CTGATATCAGAAACATGATTAATTAATGCTACATGCTTGTGGAACAGCCACTGATTCGA 2572
QY 482 GlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeuHis 501
DB 2573 GGAACAGAGAGTCCCAAGAGTTTGGTACAGGCAATTCAGATCATATGCCATGCTGCAT 2632
QY 502 AsnIleProValProGluThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSerSer 521
DB 2633 AATATCCAGAGCTGAGACCACTATCTAGGAATACACCCACCATGCCATTCAGCTCCTC 2692
QY 522 LeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIle 541
DB 2693 TTGGCCACCAACAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2752
QY 542 GlyAlaTyrAsnTyrMetGluIleGlyLysThrSerSerSerLeuAspSerThrAsn 561
DB 2753 GGAGCCATACATTTATATGAGATTTGTGGAGAGAGTTTATCATCTACTACTAGACGACAAAT 2812
QY 562 ThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer 581
DB 2813 ACGAACTTCAAG 2872
QY 582 LeuThrAspLysHisLysLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsnGly 601
DB 2873 CTGACGAGATTAACACCTGGAGCCCAATCAGGAAATCTGGGAAAGCACTGGAAAGAACTGT 2932
QY 602 AlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGluArg 621
DB 2933 GCCCGTAACCTGGGCTTCACACAGTCTCAGATTATGAAATTTGACCATGACTATGACGGA 2992
QY 622 AspGlyLeuLysGluLysValTyrGlnMetLeuGlnHisTrpValMetArgGluGlyIle 641
DB 2993 GATGAGACTGAAGAAAGAGTTTACAGATGTCTCAAAAGTGGGATGAGAGGAGGAGGATA 3052
QY 642 LysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAspLeu 661
DB 3053 AAGGAGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3112
QY 662 LeuSerSerLeuIleTyrValSerGlnAsn 671
DB 3113 CTGAGCAGCTTGATTTTACGTACGACCAAGAC 3142
RESULT 6
US-08-444-005-14


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Db      1423 -----ACAGTTGGAAACAATGATTCGATTAATCAGCATGATTT-----1461
Oy      480 AsproclThralaglyProargValTriPylarproleProserHisMetProser 499
      1462 -----GGAACTGACGTACAGAGATTGGTATCCGCAATCTTAACCAATGATATAGT 1515
Oy      500 LeuHisAnleProValProgluThrAsnTyrLeuGlyAsnThrProThrMetProPhe 519
      1516 ACTATATAAACTCCAGTCAGAGACAGACATACCGGGAAGACACACCACCATCCATAC 1575
Oy      520 SerSerLeuProPofThrAspGluSerTleLysTyrThrTleTyrAsnSerThrGlyIle 539
      1576 TTCTCTGGCCAGTACGATGACCTCAATATAATATCAATAGTTCGTGATTT 1635
Oy      540 GluInleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSer 559
      1636 CAGATTGGAAACCAATATATATGATGTTGGACTGAATCA-----CAACCA 1683
Oy      560 ThrAsnThrAsnPhelYsgluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThr 579
      1684 CCAACAACTACTTGCAGAAAGAGTGCATCTCCAGACACCAAGCCATCTTGATTAACACC 1743
Oy      580 ThrSerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisThrPlys 599
      1744 ACTAGTCTGACTGATGTAACACCTGACCTATCAGGAAAAAAGCTGGAAAGCAGTGGAAA 1803
Oy      600 AsnGlyAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyr 619
      1804 AACTGTCCCGCAAGCTGGGCTTCTCAGAGCTCTCAGATGCAATGAATCGAACCACTAT 1863
Oy      620 GluArgAspGlyLeuLysGlyLysValTyrGlnMetLeuGlnLysTyrValMetArgGlu 639
      1864 GAAAGAGATGAGTCGAAAGAGAAAGTTTACCAATTCCTTCGAAAGTGGCTATATCGGGAA 1923
Oy      640 GlyTleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnGlySerArgTle 659
      1924 GGCACCAAGGGGCGCAGTGGGAAAGTGGCCAGGACACTTCACCAATGTTGAGGATA 1983
Oy      660 AspleuLeuSerSerLeuIleTyrValSerGlnAsn 671
      1984 GACCTGCTGAACCACTTGATTCGTGCCAGCCAGAGC 2019
Db

```

RESULT 7
 US-09-328-111-495
 ; Sequence 495, Application US/09328111
 ; Patent No. 6262333
 ; GENERAL INFORMATION:
 ; APPLICANT: Endege, Wilson O.
 ; APPLICANT: Steinmann, Kathleen E.
 ; APPLICANT: Astle, Jon H.
 ; APPLICANT: Burgess, Christopher C.
 ; APPLICANT: Bushnell, Steven E.
 ; APPLICANT: Carroll III, Eddie
 ; APPLICANT: Catino, Theodore J.
 ; APPLICANT: Dertli, Adnan
 ; APPLICANT: Ford, Donna M.
 ; APPLICANT: Lewis, Marcia E.
 ; APPLICANT: Monahan, John E.
 ; APPLICANT: Schlegel, Robert
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
 ; FILE REFERENCE: CCD-257 (US)
 ; CURRENT APPLICATION NUMBER: US/09/328, 111
 ; EARLIER FILING DATE: 1999-06-08
 ; EARLIER APPLICATION NUMBER: US 60/088, 801
 ; EARLIER FILING DATE: 1998-06-10
 ; NUMBER OF SEQ ID NOS: 850
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 495
 ; LENGTH: 606
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(606)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-495

Alignment Scores:
Pred. No.: 5,89e-46 Length: 606
Score: 521.00 Matches: 99
Percent Similarity: 99.00% Conservative: 0
Best Local Similarity: 99.00% Mismatch: 1
Query Match: 14.70% Indels: 0
DB: 4 Gaps: 0

US-09-981-397a-16 (1-671) x US-09-328-111-495 (1-606)
Oy      572 TyrGlnAlaIlePheAspAsnThrThrSerLeuThrAspLysHisLeuAspProIleArg 591
      3 TACCAGACTATCTTGTGAATATACCACTAGTCTGAGGATTAACACCTGAGCAACCATCAGG 62
Oy      592 GluAsnLeuGlyLysHisTyrPlysAsnGlyAlaArgTyrLeuGlyPheThrGlnSerGln 611
      63 GAAATCTGGGAAAGCACTGGAAAAAGCTGCCCCGTAAAGTGGCTTCACACAGTCTCAG 122
Oy      612 IleAspGluIleAspHisAspTyrGluArgAspGlyLeuLysGlyLysValTyrGlnMet 631
      123 ATTGATGAATTTGACCATGACTATGACGACATGACTGAAGAGAAAGGCTTTACCAAGATG 182
Oy      632 LeuGlnLysTyrValMetArgGluGlyLysGlyAlaThrValGlyLysLeuAlaGln 651
      183 CTCCAAAAGTGGGATGAGGAGGAGGATTAAGGGAGCCAGCGTGGGAAAGCTGGCCAG 242
Oy      652 AlaLeuHisGlnGlySerArgIleAspleuLeuSerSerLeuIleTyrValSerGlnAsn 671
      243 GCGCTCCACCAAGTGTCTCGATGACCTTCTGAGCAGCTTGATTTAGTCAGCAGAAC 302
Db

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RESULT 8
 US-09-329-418-1
 ; Sequence 1, Application US/09329418
 ; Patent No. 6096539
 ; GENERAL INFORMATION:
 ; APPLICANT: ZENECA Limited
 ; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
 ; FILE REFERENCE: PHM 70536
 ; CURRENT APPLICATION NUMBER: US/09/329, 418
 ; EARLIER FILING DATE: 1999-06-11
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1873
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-09-329-418-1

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatch:	Indels:	Gaps:
2.37e-37	1873	153	100	187	156	22
Score:	448.00	Matches:	153			
Percent Similarity:	42.52%	Conservative:	100			
Best Local Similarity:	25.71%	Mismatch:	187			
Query Match:	12.64%	Indels:	156			
DB:	3	Gaps:	22			

US-09-981-397a-16 (1-671) x US-09-329-418-1 (1-1873)

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Oy      1 MetGlnProAspMetSerLeuAsnValIleLys-----11
      147 CTGGCACCCTCCACCCGATGATGCTGCTCAAGTTATGCGCCAGCGGTGCCCGCCGCC 206
Oy      12 MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyGlyPheGlyLys 30
      207 TTGCTGTCACATCGAGAACTGAGAACAGGAGAGCTCTCGCAAGCGCGGTTCCGCACA 266
Oy      31 ValSerLeuGlyPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50

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Db      267 GTGTTCCGGGCAACATAGAGTGGGC-----TACGATGTG 305
Qy      51 ProAsnGylIleGluHisAsnGluAlaLeuGluGluAlaLeuMetMetAsnArgLeu 70
Db      306 GCGGTCAAGATGCTAACTCGAAGGCGATATCCAGGAGGTCAAGCCCATGGCAAGTGTG 365
Qy      71 ArgHisSerArgValValIleuLeuGluValIleIleGluGluGly-----86
Db      366 GATACGAATTCGTCTCGCTAGAGGGGTATTCGAGAGGTGGCGGCGCCGAGCCAA 425
Qy      87 -----LysTyrSerLeuValMetLeuTyrMetGluGlyAsnLeuMetHisValLeu 104
Db      426 GATCCCAAGCCGCGCTGTGTGACTTAATTCAGAGGAACGGCTCTTCGGGGCTGTG 485
Qy      105 LysAlaGluMetSerThrProLeuSerValIleGlyArgIleIleLeuGluIleIleGlu 124
Db      486 CAGTCCCAAGTCCCTCGGCGCTGGCCCTCTTCCTTCGCGCTGTGAAGAAGTGGTCTT 545
Qy      125 GlyMetCysTyrLeuHisGlyLysGly-----ValIleHisAspLeuLysProGlu 142
Db      546 GGGATGTTTACCTGACGACCAAGAACCCGGTGTCTTCGACCCGAGCTCAAGCCATCC 605
Qy      143 AsnIleLeuValAspAsnAspPheHisIleLeuIleAlaAspLeuGlyLeuAlaSerPhe 162
Db      606 AACGTCCTGTGGACCCAGCTGCACGTCAAGCTGCAGATTGTCCTGCCACATTT 665
Qy      163 LysMetTrpSerLysLeuAsnAsnGluHisAsnGluValArgGluValAlaSerIle 182
Db      666 CAGGAGGCTCACAG-----TCAGGACA 689
Qy      183 AlaLys---LysAsnGlyIleThrLeuTyrMetAlaProGluHisLeuAsnAspVal 201
Db      690 GGGTCCGGGGGCGAGCGGCGACCTCGGCTACTTCGCGACCAAGTCTTTGTAACTGA 749
Qy      202 AsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValAlaLeuTrpAlaIle 221
Db      750 AACCGGAAGGCTCCACAGCAGGTACGTACACTTCGGGATTCATGTGGGCACTG 809
Qy      222 PheAlaAsnLysGlu-----ProTyrGlu-----AsnAlaIleCys 233
Db      810 CTTCGTGAAGAGAAGTGTAGTTCGCAACCGAACCATCACTGCTAGCAAGCACTGTGC 869
Qy      234 GluGlnGluLeuIleMetCysIleLysSerGlyAsnArgProAspValAspPheIleThr 253
Db      870 AACAGGCGAG-----AACCGGCTTCATGTGGCTGAGCTGCC 905
Qy      254 GluTyrCysProArgGlu-----IleIleSerLeuMetLysLeuCysTrp 268
Db      906 CAAAGCGGGCTGAGACTCCCGGCTTGAAGAGACTGAAGAGACTAATGCACTGTGCTGG 965
Qy      269 GluAlaAsnProGluAlaArgProThrPhe-----ProGlyIleGluLys 284
Db      966 AGCAGTAGAGCCCAAGAGACACCTCTTCAGAGATCCCTACCAAAAACGATCAACTGC 1025
Qy      285 PheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspValLysSerLeu 304
Db      1026 TTCGAG-----ATGCTGGAACAATATGATGCTGCTCTCCACGGSTA 1070
Qy      305 LysLysGluTyrSerAsnGluAsnAlaValAlaValLysArgMetGlnSerLeuGlnLeuAsp 324
Db      1071 AAGGATTTCCCTGCTCAGCTCAGAGACGACGCAATAGGACATTT-----1112
Qy      325 CysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProGlySerLeuHis 344
Db      1113 -----TCTATCCAGAGTCA-----1127
Qy      345 SerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaProSerLeuGlu 364
Db      1128 -----GGCCAAGAGGAGGACAAATGATGCTTAGAGAGAACCATAGAA 1172
Qy      365 HisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyr 384

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Db      1173 AACGAGCACTGCTGTAATGATGATGCTAGTGTCTGATGCTA-----1214
Qy      385 HisLeuTyrGlySerArgMetAspArgGlnThrLysGlnProArgGluAsnValAla 404
Db      1215 -----AACAACTGAATCTAGAGAGCCCTCCAGCTGTGTT--1250
Qy      405 TyrAsnArgGluGluGluArgArgValSerHisAspProPheAlaGlnArg 424
Db      1251 -----CCTAA-AAATGCCCGAG 1267
Qy      425 ProTyrGluAsnPheGlnAsnThrGluLysGlyThrValTyrSer-SerAlaAlaSer 444
Db      1268 CTTTACCAAGAGGAGACGAGGCAAGAGAGCAGAGCTTCACAGAGCTTGAGAGGAGCAC 1327
Qy      444 HisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrG1 464
Db      1328 ATCTTCAGATTGCGATGGCCCAACT-----CCCCAGACTCCAGAGACTTAACCTTT 1378
Qy      464 AsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAl 484
Db      1379 CAGAAACCAAGATGCCAC-----CCTACTCAACTGGAGACA--1415
Qy      484 ArgProArgValTrpTyrArgProIleProSerHisMetProSerLeuHisAsnIlePr 504
Db      1416 -----CCAAGT-----CC 1423
Qy      504 GvalProGlnThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuProPr 524
Db      1424 TGGACCCGAGGAGTAATCAGGGGCTGAGAGACAAAGCATGACTGGTCTCAGAGACCC 1483
Qy      524 ThrAspGluSerIleLys-----TyrThrIleTyrAsnSerThrGlyIleG1 540
Db      1484 GGAGCCAAATCCGTAACAGGAGCGACCGCTCGTTAACTATATACAACTGCTCGGGGTCA 1543
Qy      540 nIleGlyAlaTyrAsnTyrMetGluIleGlyIleThrSerSer 554
Db      1544 AGTTGGAGACAACAACACTTGTGACTATGCAACAGCAACTGCC 1586

RESULT 9
US-09-531-914-1
; Sequence 1, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531,914
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1873
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-531-914-1

Alignment Scores:
Pred. No.: 2,37e-37 Length: 1873
Score: 448.00 Matches: 153
Percent Similarity: 42.52% Conservative: 100
Best Local Similarity: 25.71% Mismatches: 187
Query Match: 12.64% Indels: 156
DB: 4 Gaps: 22

US-09-981-397A-16 (1-671) x US-09-531-914-1 (1-1873)
Qy      1 MetGlnProAspMetSerLeuAsnValIleLys-----11
Db      147 CTGGACCTTCCACGCTGATGTCGTGGCTCAAGTTATAGCCCGAGCGGTGCCCCCCCC 206
Qy      12 MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyGlyPheGlyLys 30

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Db 207 TTGGTGTCCATCGGAGACTGGAGAACAGAGCTCTGGCAAGCGGGCTTGCGACA 266
Qy 31 ValSerLeuCySPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50
Db 267 GTGTCCGGGGCGCAACATAGGAAGTGGGC-----TACGATGTG 305
Qy 51 ProAsnGlyIleGlnHisAsnGlnAlaLeuGlnGlnAlaLysMetMetAsnArgLeu 70
Db 306 GCGGTCAAGATCGTAACCTGCAAGCGCATATCCAGGAGGTCAAGGCCATCGCAAGTGTG 365
Qy 71 ArgHisSerArgValValLysLeuGlnGlyAlaIleIleGlnGlyGly----- 86
Db 366 GATACCAATTCGTGCGCGCTTAGAAGGCTATTCAGAAAGTTCGGGCGCTCGAGCCAA 425
Qy 87 -----LysTyrSerLeuValMetGlnTyrMetGlnLysGlnAsnLeuMetHisValLeu 104
Db 426 GATCCCAAGCGCGCTGTGTGACTAAATTCATGGAGAACGGCTCTGTGTGCGGGCTGTG 485
Qy 105 LysAlaGlnMetSerThrProLeuSerValLysGlnArgIleIleLeuGlnIleIleGln 124
Db 486 CAGTCCCAAGTGGCTGTGGCCCTGTGGCTCTTGGCCGCTGGAAGAAGTGTGTGCTT 545
Qy 125 GlyMetCysTyrIleuHisGlyLysGly-----ValIleHisLysAspLeuLysProGln 142
Db 546 GGGATGTTTACCTCCAGACACGACACACCGGCTGCTCTGACCGAGCATCAAGCCATCC 605
Qy 143 AsnIleLeuValAspAsnAspPheHisIleLysIleLeuAspLeuGlnLysLeuAlaSerPhe 162
Db 606 AACCTCTGCTGGAGCCAGACGTGCACGTGCAATTTGTCCTCCACATTT 665
Qy 163 LysMetLysSerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgGlnValAspGlyThr 182
Db 666 CAGGAGAGCTCACAG-----TCAGGAGCA 689
Qy 183 AlaLys---LysAsnGlyGlyThrLeuTyrTyrMetAlaProGlnHisLysAsnAspVal 201
Db 690 GGGTCCGGGAGGAGGGGCGACCCCTGGCTACTTGGCCCGCAAGCTTTGTTAAAGCTA 749
Qy 202 AsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValAlaLeuThrAlaIle 221
Db 750 AACCGGAAGGCTCTCACAGCCAGTACGCTTACAGCTTCCGGATCTTAATGTGGGACGTG 809
Qy 222 PheAlaAsnLysGln-----ProTyrGln-----AsnAlaIleCys 233
Db 810 CTTCCTGGAGAGAGAGTGAAGTTCACACGAAACCATCATCCTGTACAGAGAGCTGTGC 869
Qy 234 GlnGlnGlnLeuIleMetCysIleLysSerLysAsnArgProAspValAspAspIleThr 253
Db 870 AACAGGCGAG-----AACCGGCTTCAATTGGCTGAGACTGCC 905
Qy 254 GlnTyrTyrProArgGln-----IleIleSerLeuMetLysLeuCysTyr 268
Db 906 CAACCCGGGCTGTGAGACTCCCGGCTTAGAAGAGCTGAAGAGCAATATGCTGCTCCACGCTA 965
Qy 269 GlnAlaAsnProGlnAlaArgProThrPhe-----ProGlyIleGlnGlnLys 284
Db 966 AGCAGTGAAGCCCAAGAGACAGCCCTCTCCAGCAATGCCCTACCAAAAACGATGAAGTCT 1025
Qy 285 PheArgProPheTyrLeuSerGlnLeuGlnGlnSerValGlnGlnAspValLysSerLeu 304
Db 1026 TTCAG-----ATGCTGAGAGAACATATGATGCTGCTGCTCCACGCTA 1070
Qy 305 LysLysGlnTyrSerAsnGlnAlaValAlaValLysArgMetGlnSerLeuGlnLeuAsp 324
Db 1071 AAGGATTTCTGTCTGCTCAGCTCAGAGACAGCAATAGGAGATTT----- 1112
Qy 325 CysValAlaValProSerSerArgSerAsnSerAlaThrGlnGlnProGlySerLeuHis 344
Db 1113 -----TCATATCCAGAGTCA----- 1127
Qy 345 SerSerGlnGlyMetGlyProValGlnGlnSerTyrPheAlaProSerLeuGln 364

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Db 1128 -----GCCCAAGAGGAGACAGAAATGATGGCTTTAGAGAACCATAGAA 1172
Qy 365 HisProGlnGlnGlnAsnGlnProSerLeuGlnSerLysLeuGlnAsnGlnAlaAsnTyr 384
Db 1173 AACGAGACACTCTGTAATGATGATGATGTTCTTAGTGGCTA----- 1214
Qy 385 HisLeuTyrGlySerArgMetLysAspArgGlnThrLysGlnGlnProArgGlnAsnValAla 404
Db 1215 -----AACAACTGATCTAGAGAGGAGCTCCAGCTGTGTT--- 1250
Qy 405 TyrAsnArgGlnGlnGlnArgArgArgValSerHisAspProPheAlaGlnGlnArg 424
Db 1251 -----CCTAA-AAATGCCGAG 1267
Qy 425 ProTyrGlnAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer-SerAlaIle 444
Db 1268 CTTTACCAAGAGGAGGAGGAGACAGAGAGAGAGAGCTTCCACAACTCTGGAGACGAGCAC 1327
Qy 444 HisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGln 464
Db 1328 ATCTTCAGATTCGATGGCCCAACT-----CCCAAGACCTCCAGAGACTCAACTTT 1378
Qy 464 AsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAl 484
Db 1379 CAGAAACAGATGCGCCAGC-----CCTACCTCACTGGAACA-- 1415
Qy 484 aglyProArgValIrrpyrArgProIleProSerHisMetProSerLeuHisAsnIlePr 504
Db 1416 -----CCAGT-----CC 1423
Qy 504 oValProGlnThrAsnTyrLeuGlnGlyAsnThrProThrMetProPheSerSerLeuProPr 524
Db 1424 TGGACCCCGAGGAGATCAGGGGCTGAGAGACAGAGCATGACGTCTCTCCAGAGACC 1483
Qy 524 cThrAspGlnSerLys-----TyrThrIleTyrAsnSerThrGlyIleGln 540
Db 1484 GGACCCAAATCCACTACAGGCGAGCGCTGTTAAATACATACATGCTCTGGGGTGA 1543
Qy 540 nileGlyAlaTyrAsnTyrMetGlnIleGlyGlyThrSerSer 554
Db 1544 AGTTGAGACACAACTACTTGTACTATGCAACAGACAACTGCC 1586

```

RESULT 10
 US-09-329-418-2
 : Sequence 2, Application US/09329418
 : Patent No. 6096539
 : GENERAL INFORMATION:
 : APPLICANT: ZENECA Limited
 : TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
 : FILE REFERENCE: PHM.70536
 : CURRENT APPLICATION NUMBER: US/09/329,418
 : CURRENT FILING DATE: 1999-06-11
 : NUMBER OF SEQ ID NOS: 39
 : SOFTWARE: FASTSEQ for Windows Version 3.0
 : SEQ ID NO 2
 : LENGTH: 1557
 : TYPE: DNA
 : ORGANISM: Homo Sapiens
 US-09-329-418-2

Alignment Scores:
 Pred. No.: 2,79e-37 Length: 1557
 Score: 446.00 Matches: 150
 Percent Similarity: 43.01% Conservative: 96
 Best Local Similarity: 26.22% Mismatches: 181
 Query Match: 12.58% Indels: 146
 DB: 3 Gaps: 21

US-09-981-397a-16 (1-671) x US-09-329-418-2 (1-1557)
 Qy 14 SerSerAspPheLeuGlnSerAlaGlnLeu---AspSerGlyGlyPheGlyLysValSer 32
 Db 49 TCCATCGAGAACTGGAGAACACAGAGCTGTGCGCAAGGCGGCTTCGCGACAGTGTTC 108

```

OY 33 LeucySpheHsArgThrGlnGlyLeuMetIleMetLysThrValTyrIlySgLYProasn 52
Db CGGCGCAACATAGAGAGTGGGC-----TACATGTGGCGGTC 147
OY 53 CysIIleGlnHsAsnGlnAlaLeuLeuGlnGlnAlaLysMetMetAsnArgLeuArgHis 72
Db 148 AAGATCGTAAACTCCAGGCGCATATCCAGGAGGTTCAGGCGCATGCGCAATGTGATTAAC 207
OY 73 SerArgValIValIleuLeuGlyValIle-----IleGlnGlnGlyLys 87
Db 208 GAATTCGTCGTCGCTGAGAGGGGTATCCGAAGGTCAGTACGGAGCCCAAGATCCCAAG 267
OY 88 TyrSerLeuValMetGlnTyrMetGlnLysGlyAsnLeuMetHisValLeuLysAlaGln 107
Db 268 CCGGCTGTGTCGACTAAATTCATGAGAAAGCGCTCTGTGCGGGCTGCTGACAGTCCAG 327
OY 108 MetSerThrProLeuSerValLysGlyArgIleIleLeuGlnIleIleGlnGlyMetCys 127
Db 328 TGCCCTGAGCCCTGGCCGCTCTTCCGCTGCTGAAAGAGTGTGCTGGATGTTT 387
OY 128 TyrLeuHsIlySgLYsGly-----ValIleHsIlyAspLeuLysProGlnAsnIleLeu 145
Db 388 TACCTGCAGACACCAACACCGGCTGCTGCGACCGGAGCTCAACCATCCACACTCTG 447
OY 146 ValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLysMetTrp 165
Db 448 CTGGACCCAGAGCTCAGCTCAAGCTGAGAGATTTGGCTGTCCACATTCAGGAGAGC 507
OY 166 SerLysLeuAsnAsnGlnGlnHsAsnGlnLeuArgGlnValAspGlyThrAlaLys--- 184
Db 508 TCACAG-----TCAGGACAGGCGTCCGG 531
OY 185 LysAsnGlyGlyThrLeuTyrMetAlaProGlnHsIleAsnAspValAsnAlaLys 204
Db 532 GAGCAGAGGGGACCTGGCTGCTGCGACCGGAGCTCAACCATCCACACTCTG 447
OY 205 ProThrGlnLysSerAspValTyrSerPheAlaValIleTrpAlaIlePheAlaAsn 224
Db 592 GCCTCCACAGCAGTACGCTACAGCTCGGATCTGAATGTGGGAGTCTGCTCGA 651
OY 225 LysGln-----ProTyrGln-----AsnAlaIleCysGlnGln 236
Db 652 AGAGAGTGTGAGTCCCAACCGACCATCTGTGTCAGAGAGTGTGCAACAGGAG 711
OY 237 LeuIleMetCysIleLysSerGlyAsnArgProAspValAspAspIleThrGlnTyrCys 256
Db 712 -----AACGGCTTATTTGGCTGAGACTGCCCAACCGGG 747
OY 257 ProArgGln-----IleIleSerLeuMetLysLysCysTrpGlnAlaAsn 271
Db 748 CCTGAGACTCCCGCTTAGAAGAGTGAAGAGTAATGACAGCTGTGCGAGAGTGA 807
OY 272 ProGlnAlaArgProThrPhe-----ProGlyIleGlnGlnLysPheArgPro 287
Db 808 CCCAAGGACAGACCTCTCCAGAGATGCTTCAACAAAAGTGAAGTGTCCAG--- 864
OY 288 PheTyrLeuSerGlnLeuGlnGlnSerValGlnGlnAspValLysSerLeuLysGln 307
Db 865 -----ATGGTGGAGACAAATGATGCTGCTGTCTCCACGGTAAAGATTTTC 912
OY 308 TyrSerAsnGlnAsnAlaValIleValIleValIleValIleValIleValIleValIle 327
Db 913 CTGTCCTCAGCTCAGAGCAGCAATAGAGATTT-----TCT 948
OY 328 ValProSerSerArgSerAsnSerIleThrGlnGlnProGlySerLeuHsIserSerGln 347
Db 949 ATCCAGAGTCA----- 960
OY 348 GlyLeuGlyMetGlyProValGlnGlnSerTrpPheAlaProSerLeuGlnHsIProGln 367
Db 961 -----GGCCAAAGAGGAGCAGAAATGATGCTTTAGACAGACCATAGAAAACACAGAC 1014

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OY 368 GlnGlnAsnGlnProSerLeuGlnSerLysLeuGlnAspGlnAlaAsnTyrHisLeuTyr 387
Db 1015 TCTCGTAATGATGTCATGTTCTGTAGTGGCTA----- 1047
OY 388 GlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArg 407
Db 1048 -----AACAACTGAATCTAGAGGAGCCCTCCAGCTGTT----- 1083
OY 408 GlnGlnGlnArgArgArgValSerHisAspProPheAlaGlnGlnArgProTyrGln 427
Db 1084 -----CCTAA-AAATATCCCGAGGCTTTACCA 1109
OY 428 AsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer-SerAlaAlaSerHisGlyAs 447
Db 1110 GAGGAGCAGGCGCACAAGAGAGACAGGTTCACACCTGAGACAGCAGCATCTTCAGA 1169
OY 447 nAlaValHsGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAsnArg 467
Db 1170 TTGATGAGGCCCAACT-----CCCGAGACTCAGAGACCTCACTTCAGAAACA 1220
OY 467 yLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaGlyProArg 487
Db 1221 GATGCCACG-----CTTACTCACTGGAACA----- 1248
OY 487 gValTrpTyrArgProIleProSerHisMetProSerLeuHisAsnIleProValProGln 507
Db 1249 -----CCAGT-----CTGGACCCCG 1265
OY 507 uThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuProProThrAspGln 527
Db 1266 AGGGAATCAGGGGCTGAGACAGACAGCATGAACGTGTCCTCCAGACCCCGAGCCAAA 1325
OY 527 uSerIleLys-----TyrThrIleTyrAsnSerThrGlyIleGlnIleGlyAl 543
Db 1326 TCCATACACAGGCGCAGCGCTGTTACATATACATACACTGCTGTGGGTGTCANATTGGAGA 1385
OY 543 aTyrAsnTyrMetGlnIleGlyGlyThrSerSer 554
Db 1386 CAACAACACTTACTGACTATGCAACAGACAACTGCC 1419

RESULT 11
US-09-531-914-2
; Sequence 2, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531.914
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-531-914-2

Alignment Scores:
Pred. No.: 2.79e-37 Length: 1557
Score: 446.00 Matches: 150
Percent Similarity: 43.01% Conservative: 96
Best Local Similarity: 26.22% Mismatches: 181
Query Match: 12.36% Indels: 146
DB: 4 Gaps: 21

US-09-981-397A-16 (1-671) x US-09-531-914-2 (1-1557)
OY 14 SerSerAspPheLeuGlnSerAlaGlnLeu---AspSerGlyGlyPheGlyLysValSer 32
Db 49 TCCATCGAGGAACCTGAGACACAGAGCTCTCGCCAAAGGCGGGTTTCGACACAGTCTTC 108

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OY	33	LeucysPheHisAspGlyThrGlnILeuMetIleMetLysThrValTyrLysGlyProAsn	52
Db	109	CGGGCGCAACAATAGAAAGTGGGC-----TACGATGTGGCGTC	147
OY	53	CysIleGlnHisAsnGlnAlaLeuLeuGlnGlnAlaLysMetMetAsnArgLeuArgHis	72
Db	148	AAGATCGTAAACTCGAAGCGCATATCCAGGAGGTCACAGGCCATGGCAATGCTGGATTAAC	207
OY	73	SerArgValValLysLeuGlnGlyValIle-----IleGlnGlnLysLys	87
Db	208	GAATTCGTGCTGGCGCTTGAAGGGGTTTATCGAAGAGTGAACGTGGACCAAGATCCCAAG	267
OY	88	TyrSerLeuValMetGlnTyrMetGlnLysGlyAsnLeuMetHisValLeuLysAlaGlu	107
Db	268	CCGGCTGTGGTGACAAATTCATGAGAGAACGGCTCTCTGTGGGGCTCTCTGCAGTCCAG	327
OY	108	MetSerThrProLeuSerValLysGlyArgIleIleLeuGlnIleIleGlnGlyMetCys	127
Db	328	TGCCCTTGGCCCTGGCCGCTCTTGTCCGCTCGAAGAAAGTGGTCTTGGGATCTTT	387
OY	128	TyrLeuHisGlyLysGly-----ValIleHisLysAspLysProGlnAsnIleLeu	145
Db	388	TACTGCGACGACCAACACCGGTGCTCTCTGACCGGAGCTCAACCCATCCAACTCTGTG	447
OY	146	ValAspAsnAspPheHisIleLysIleAlaAspLeuGlnLeuAlaSerPheLysMetTrp	165
Db	448	CTGGACCCAGAGCTGCACGTCAAGCTGCACAGATTGTCGCTCCACATTTCAGGAGAGC	507
OY	166	SerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgGlnValAspGlyThrAlaLys---	184
Db	508	TCACAG-----TCAGGACAGGGTCCGGC	531
OY	185	LysAsnGlnGlyThrLeuTyrTyrMetAlaProGlnHisLeuAsnAspValAsnAlaLys	204
Db	532	GAGCCAGGGGGACCCCTGGCTACTGGCCCCAGACGTTTGTTAACGTAAACCGGAG	591
OY	205	ProThrGlnLysSerAspValTyrSerPheAlaValLeuTyrPalaIlePheAlaAsn	224
Db	592	GCCCTCCACAGCAGTGCAGCTTACAGCTCGGAGCTCAAGTGGGGCAGTCTTCTTGGA	651
OY	225	LysGln-----ProTyrGln-----AsnAlaIleCysGlnGlnGln	236
Db	652	AGAGAGATGAGTTGCCAACCGAACCATCACTCGTGTACGAGACAGTGTGCACACGGGAC	711
OY	237	LeuIleMetCysIleLysSerGlyAsnArgProAspValAspAspIleThrGlnTyrCys	256
Db	712	-----AACCGGCTTCATTGGGTGAGCTCCCCAAACCGCG	747
OY	257	ProArgGln-----IleIleSerLeuMetLysLeuCysTyrPalaAsn	271
Db	748	CCTGAGACTCCCGGCTTAGAAGAGACTGAAGAGACTGAATGACAGCTCTGTCGAGCAGTGTAG	807
OY	272	ProGlnAlaArgProThrPhe-----ProGlyIleGlnLysLysPheArgPro	287
Db	808	CCCAAGACACACCTCTCTCCAGAGATGCTTACCACAAAACGTGATGAAGTCTTCAG--	864
OY	288	PheTyrLeuSerGlnLeuGlnGlnLysSerValGlnGlnAspValLysSerLeuLysGln	307
Db	865	-----ATGCGTGAGAACAAATGTGAATGCTGCTGCTCCACCGTAAAGAGATTTC	912
OY	308	TyrSerAsnGlnAsnAlaValValLysArgMetGlnSerLeuGlnLeuAspCysAlaAla	327
Db	913	CTGTCTCAGCTCAGCAGCAGCAATATGGAGATT-----TCT	948
OY	328	ValProSerSerArgSerAsnSerAlaThrGlnGlnProGlySerLeuHisSerSerGln	347
Db	949	ATCCACAGATCA-----	960
OY	348	GlyLeuGlnMetGlyProValGlnGlnSerTrpPheAlaArgProSerLeuGlnHisProGln	367
Db	961	-----GGCCAAAGGAGGACGAATATGGATGGCTTTAGAGAACCATGTGAATAACGAGAC	1014

QY	368	GlUGluGInaAngIuPProSerLeGInserLysLeuGInaSPuGuaIaIaSnTyHnISLeuTyT	387
Db	1015	TCTCGTAAFGATGTCATGATGTTTCGACGGCTA	1047
QY	388	GLYSerArGmetAsPaRgInThrLysGInGInProArGInaSnVaIaIaTyRAsnaRg	407
Db	1048	-----AACAAACGTAAACCTAGAGGAGCGCTCCACCTCTGTT-----	1083
QY	408	GLUGluGInaArGArGArGArGValSerHisAsProPheIaGInGInaRProTyGlu	427
Db	1084	-----CCTAA-AAAATGCCGACCTTATCCAA	1109
QY	428	AsnPheGInaSnThrGluGlyLysGlyThrValTyrSer-SerAlaIaSerHisGlyAs	447
Db	1110	GAGCAGCCAGGGCCACAGAGGACAGGATCCCAAAACCTCGCAACGACGACCATCTTCAGA	1165
QY	447	nAlaVaIaHsGInProSerGlyLeuThrSerGInProGInValLeuTyRgInaSnG	467
Db	1170	TTTCGATGGCCCAACT-----CCCAACACTCCAGACACCTCAACTTTCAGAAACCA	1220
QY	467	YLeuTyRSerSerHisGlyPheGlyThrArGProLeuAsPProGlyThrAlaGlyProAr	487
Db	1221	GATGCCCGAC-----CCTAACCTCAACTGGACAA	1248
QY	487	gValTrpYrAlaRProIleProSerHisMetProSerLeuHIsaNIleProValProG	507
Db	1249	-----CCAAGT-----CCTGCACCCG	1265
QY	507	uThrAsnTyRLeuGlyAsnThrProThrMetProPheSerSerLeuProThrAsP	527
Db	1266	AGGGATCATGGGGGCGGTAGACACAAGCAGTAACTGGTCCGCAAGACCCGAGCCAAA	1325
QY	527	uSerIleLys-----TyrThrIleTyRAsnSerThrGlyIleGInIleGlyAl	543
Db	1326	TCCAGTACAGGGCCACCGCCTCGTTAACATATACAACTGCTGGGGTGCAAAGTTGGAGA	1385
QY	543	aTyRAsnTyRmetGluIleGlyGlyThrSerSer	554
Db	1386	CACACACTACTTGACTATGCAACAGACACTGGCC	1419
RESULT 12			
US-09-188-930-257			
Sequence 257, Application US/09188930A			
Patent No. 6150502			
GENERAL INFORMATION:			
APPLICANT: Watson, James D.			
APPLICANT: Strachan, Lorna			
APPLICANT: Sleeman, Matthew			
APPLICANT: Onrust, Rene			
TITLE OF INVENTION: Compositions Isolated From Skin Cells			
FILE REFERENCE: 11000.1011c1			
CURRENT APPLICATION NUMBER: US/09/188,930A			
CURRENT FILING DATE: 1998-11-09			
NUMBER OF SEQ ID NOS: 348			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 257			
LENGTH: 3516			
TYPE: DNA			
ORGANISM: Mouse			
US-09-188-930-257			
Alignment Scores:			
Pred. No.: 6.82e-33			
Score: 410.50			
Percent Similarity: 43.43%			
Best Local Similarity: 28.72%			
Query Match: 11.58%			
Db: 3			
Length: 3516			
Matches: 164			
Conservative: 84			
Mismatches: 209			
Indels: 116			
Gaps: 25			
US-09-981-397A-16 (1-671) x US-09-188-930-257 (1-3516)			

[illegible]

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Db      1045  ACTCTTGAAGAGCCCGGAAGAGCTAGCCGGAAGTTCTCTGATGACAGACTCCATCTGCC 1104
QY      381  GUAUAasnTYrHisLeuTYrGLY--SerArgMetAspArgGlnTYrLYsGlnGlnPro 399
Db      1105  AGCAGTGCACAGAGAGCTCTCGGGGGGTGCTCCAGAGGACTCAGAGCTTTTCTCCAGAGA 1164
QY      400  ArgGlnAsnValAlaTYrAsnArgGlnGlnGlnGlnArgGlnGlnGlnGlnGlnGlnGln 419
Db      1165  TCGCTGTACTGTCTTTTGAAGCGGGAGACTTC-AACAGGCA-----CCT 1208
QY      420  PheAlaGlnGlnArgProTYrGluAsnProPheGlnAsnThrGlnGlnLYsGlnTYrValTYr 439
Db      1209  GGGCCCCACAGACATCCAGAGA-----GAAAGTACGATGCCATCAT 1253
QY      440  SerSerAlaAlaSerHisGlnLYsAsnAlaValHisGlnProSer-----GlyLeu 455
Db      1254  -----ATCAGGGGACACCAGAGCTGATGAGATCTCTACAGCCCCAAGATGTGGACTT 1307
QY      456  ThrSer----- 457
Db      1308  GGTTCAGACAGCACTGCCAGCTCTGTGCACTTGTGGAGCCGGACAGGAGAGTGTG 1367
QY      458  -----GlnProGlnValLeuTYrGlnAsnAsnGlyLeu 468
Db      1368  TGTCAAGTGGCTGCTGCTTAACAAATGCCAACCCCACT---GACCAACAGAGAGGGCTC 1424
QY      469  Tyr---SerSerHisGlnPheGlnTYr----- 476
Db      1425  TACACACTGCATATGATGCTGTGAGCGGAGAGGAGCTGGAATTGTGGAGTACTGTAGC 1484
QY      477  -----ArgProLeuAsp--ProGlyThrIleArg 486
Db      1485  CCGGAGACCACTGTCAATGCCAAGATGAAGACCAAGTGCCTGCTGCACTTGGACG 1544
QY      486  roATValTYrTYrArgProIleProSerHisMetProSerLeuHisAsnIleProValP 506
Db      1545  CCAGATAGGGGATGAGCCACACAGAGCTG-CGTGTAGAG--AAGATGCTTCTGTCA 1600
QY      506  roGlnTYrAsnTYrLeuGlnLYsAsnIlePro 515
Db      1601  ATGAGTGGACTTGTGAGGGCCGAACACC 1629

RESULT 13
US-09-188-930-66
; Sequence 66, Application US/091889930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 1888
; TYPE: DNA
; ORGANISM: mouse
FEATURE:
; NAME/KEY: unsure
; LOCATION: (1690)...(1690)
; NAME/KEY: unsure
; LOCATION: (1755)...(1755)
; NAME/KEY: unsure
; LOCATION: (1864)...(1864)
US-09-188-930-66

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Alignment Scores:

Pred. No.: 1,17e-29 Length: 1888
 Score: 375.50 Matches: 156
 Percent Similarity: 41.86% Conservative: 83
 Best Local Similarity: 27.32% Mismatches: 219
 Query Match: 10.59% Indels: 115
 DB: 3 Gaps: 26

US-09-981-397a-16 (1-671) x US-09-188-930-66 (1-1888)

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QY 14 SerSerAspPheLeuGluSerAlaGluLeuAspSerGlycylPheGlyLysValSerLeu 33
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
58 GCGCGCAATTCCTCCAGCTGGAGAAAGTGGCTCGCGCTCGCGGAGCTGACAG 117
QY 34 CysPheHisArgThrGlnGlyLeuMetLleMetLysThr-----ValTyrLysGly 50
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
118 GTCCGCCAT-----GTGCACTGGAGACGTGGCTCGCGCAACTGCTCG 162
QY 51 ProAsnGlyS-----LleGluHisAsnGlu-----AlaLeuLeuGluAlaLysMetMet 67
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
163 CCCAGTCTGCACGTCGACGACAGCAAGCAATGAGAGCTCGTGGAGAGCAAGTAAAGATG 222
QY 68 AsnArgLeuArgHisSerArgValValLysLeuLeuGlyValLleleGluGluGlyLys 87
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
223 GAGATGGCCAAATTCGATACATCTACCTGTACGCGCATATGCCAGAA-----CCT 276
QY 88 TyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLysAlaGlu 107
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
277 GTGCGCTGTGTCATGGATGATGATGAGACAGAGCTCCCTGGAGAAAGCTGGCTCGACAG 336
QY 108 MetSerThrProLeuSerValLysGlyArgLleleLeuGluLleleleGluGlyMetCys 127
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
337 ---CAATGGCTTGGGACCTGGCTTTCGATCGTGCAGACAGACGCCGTGGCATAC 393
QY 128 TyrLeuHis-----GlyLysGlyValLleHisLysAspLeuLysProGluAsnLleLeu 145
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
394 TTCTCTCATGTGATGTCTCCGCCCATGCTCCATACCTGAAGCCAGGACATCTTG 453
QY 146 ValAspAsnAspPheHisLle-----LysLleAlaAspLeuGlyLeuAlaSerPheLysMet 164
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
454 CTGGATGCCCACTACCAATGTCAGAGATTTCTTGACTTGGCGTGGCC----- 501
QY 165 TrpSerLysLeuAsnAsnGluGluHisAsnGluLeuArgLysValAspGlyThrAlaLys 184
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
502 -----AGTGCATATGCGATGTCCTCCACTGTACGACTCAGCATGATGAGCTGTT--- 552
QY 185 LysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAsnAlaLys 204
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
553 -----GTTCAATTCGGCTACCTCCCTCCCTCAGAGCAATTCGTGAGAGAGCCGCTTG 603
QY 205 ProThrGluLysSerAspValTyrSerPheAlaValValLeuThrPheAlaLlePheAlaAsn 224
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
604 TTTGACACCAAAATGATGATATACAGCTTGCCATTGTGATGTGGGTGATTCACAG 663
QY 225 LysGluProTyrGluLysAlaLleCysGluGluGluLeuLeuMetCysLleLysSerGly 244
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
664 AATATTCATTCATTCAGATGAAGAAACATCTACACATCTATGATGAAGTGAAGGC 723
QY 245 AsnArgProAspValAspAspLleThrGluTyrCysProArg-----GluLleLle 261
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 CACCGCCCAAGATGCTGCACCATCTCAGACCCCGCGGTGCTGCTGTCAGACCTGATA 783
QY 262 SerLeuMetLysLeuGlyTrpGluAlaAsnProGluAlaArgProThrPheProGlyLle 281
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
784 GGGCTATGCAAGCGTGTGGCATGCAAGCCACAGCTGGGCGCCACCTTCCAGAAAT 843
QY 282 GluGluLysPheArgProPheTyrLeuSerGluLeuSerGluValGluLysVal 301
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
844 ACCTGTGA-----ACAGAGACCTTTGTGAGAAAGCTGATGAGAGAGCTG 888
QY 302 LysSerLeuLysGlyTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeu 321
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
889 AAGAGCTGTGCTCATGAGCCAGGCGAGAAAGC-----TCTCTA 927

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QY 322 GlnLeuAspCysValAlaValPro---SerSerArgSerAsnSerAlaThrGluGlnPro 340
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
928 GAGTCCCAAGATGAGGCCAGGCCGAGTCTCCACGCTTCAAGCGCCCTGCTCCCCC 987
QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerThrPheAla 360
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
988 TTTCATTAACGACGTCTCTCTCCGACTTGTCTGATCAGATTTGAGACTCTGGGATTTCCA 1047
QY 361 ProSerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeu---Gln 379
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1048 AGACTCTTGAAGAGCCCGCAAGAGCTCAGCGAAGTTCTCTGATGATCAAGCTCCATCG 1107
QY 380 AspGluAlaAsnTyrHisLeuTyrGly---SerArgMetAspArgGlnThrLysGlnGln 398
DB      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1108 TTCACAGATGGCAAGAGCTCTCGGGGTCTCCATGATGATCAAGCTTTTCTCCAGA 1167
QY 399 ProArgGlnAsnValAlaTyrAsnArgGluGluGluArgArgArgValSerHisAsp 418
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1168 GGAATCGCTGTACATCTCTTTGACGGGAAAGCTTC-AAACAGCGCA----- 1211
QY 419 ProPheAlaGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrVal 438
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1212 CCTGGGCCCAACAGACATCCAGAGAA-----GAAGCTAGCGATGCCAT 1256
QY 439 TyrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSer-----Gly 454
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1257 CAT-----ATCAGGGACACACAGAGCTGATGATGATCTTACAGCCCAAGATGTGA 1310
QY 455 LeuThrSer----- 457
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1311 CTTCGTCTTACAGACAGAGTGCACAGCTGCTGCACACTGTGTGAGGCCGAGACAGAGA 1370
QY 458 -----GlnProGlnValLeuTyrGlnAsnAsnGly 467
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1371 GTGTGTCAAGTGGCTGCTGTTAAACAATGCCAACCCCAACT---GACCAACAGAGAGG 1427
QY 468 LeuTyr---SerSerHisGlyPheGlyThr----- 476
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 477 -----ArgProLeuAsp---ProGlyThrAla 484
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1488 AGCCCGGAACACAGTGTCAATGCCAAGATGAAGACAGAGTGCCTGCTGCACTTGC 1547
QY 485 GlyProArgValTyrTyrArgProLleProSerHisMetProSerLeuHisAsnLlePro 504
DB      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 505 ValProGluThrAsnTyrLeuGlyAsnThrPro 515
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1604 GTCAATGAGGTGAGCTTGAAGGCCGAACACC 1636

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RESULT 14
 US-09-099-041A-3
 : Sequence 3, Application US/09099041A
 : Patent No. 6340576
 : GENERAL INFORMATION:
 : APPLICANT: Bertin, John
 : TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
 : TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
 : FILE REFERENCE: 07334-076001
 : CURRENT APPLICATION NUMBER: US/09/099, 041A
 : PRIOR FILING DATE: 1998-06-17
 : PRIOR APPLICATION NUMBER: 09/019, 942
 : NUMBER OF SEQ. ID NOS: 37
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ. ID NO 3
 : LENGTH: 1620
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 US-09-099-041A-3


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DB 427 CTTCATCATGACTGACATCAGATCATCTTATGTGACAAATGAATTCATCTTAAGATT 486
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OY 372 ProSerLeuGIuSerLysLeuGIuAsp 380
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Search completed: June 25, 2003, 22:32:20
Job time : 154 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame-plus.p2n model

Run on: June 25, 2003, 21:59:04 ; Search time 239 Seconds
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4119.848 Million cell updates/sec

Title: US-09-981-397A-16

Perfect score: 3545
Sequence: 1 MQPMSLVNVIKMSDFLES.....ALHOCSTRIDLSLIYVSQN 671

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Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

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Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3545	100.0	2617	9	US-09-981-397A-15	Sequence 15, Appl
3	772	21.8	529	9	US-09-854-133-676	Sequence 676, App
4	641	18.1	392	9	US-09-918-995-17425	Sequence 17425, A

	C	5	538	15.2	331	9	US-09-796-692-6140	Sequence 6140, Ap
	6	538	15.2	331	9 <td>US-10-040-862-6140</td> <td>Sequence 6140, Ap</td>	US-10-040-862-6140	Sequence 6140, Ap	
	7	521	14.7	606	10	US-09-879-536-495	Sequence 495, App	
	8	463	13.1	430	10	US-09-960-352-4340	Sequence 4340, Ap	
	9	445.5	12.6	2111	9	US-10-198-846-13921	Sequence 13921, A	
	10	440	12.4	1697	10	US-09-862-027-7	Sequence 7, Appl	
	11	410.5	11.6	2370	9	US-10-164-080-1	Sequence 1, Appl	
	12	410.5	11.6	3516	9	US-10-299-327-1	Sequence 1, Appl	
	13	410.5	11.6	3516	9	US-10-152-661-257	Sequence 257, App	
	14	410.5	11.6	3516	9	US-09-866-050A-257	Sequence 257, App	
	15	409.5	11.6	1700	9	US-10-152-661-510	Sequence 510, App	
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	17	408.5	11.5	1774	9	US-10-152-661-403	Sequence 403, App	
	18	408.5	11.5	1774	9	US-09-866-050A-403	Sequence 403, App	
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	20	403.5	11.4	2255	9	US-10-164-080-6	Sequence 6, Appl	
	21	375.5	10.6	1888	9	US-10-152-661-66	Sequence 66, Appl	
	22	375.5	10.6	1888	9	US-09-866-050A-66	Sequence 66, Appl	
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	24	371	10.5	1620	10	US-09-728-721-3	Sequence 3, Appl	
	25	371	10.5	1620	12	US-10-105-931-3	Sequence 3, Appl	
	26	371	10.5	1620	12	US-10-105-931-3	Sequence 3, Appl	
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	28	371	10.5	1931	10	US-09-748-537-2	Sequence 2, Appl	
	29	371	10.5	1931	12	US-10-133-780-2	Sequence 2, Appl	
	30	371	10.5	1931	12	US-10-105-931-1	Sequence 1, Appl	
	31	371	10.5	2501	9	US-09-981-397A-13	Sequence 13, Appl	
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	40	332	9.4	5180	10	US-09-880-107-3668	Sequence 3668, Ap	
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	45	320.5	9.0	6383	9	US-09-954-531-405	Sequence 405, App	

ALIGNMENTS

RESULT 1
US-09-758-003-1
; Sequence 1, Application US/09758003
; Patent No. US20020098522A1
GENERAL INFORMATION:
APPLICANT: BAICHWAL, VIJAY R
HUNG, JIANNING
HSU, HAILING
GOEDDEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
ASSAYS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758, 003
FILING DATE: 09-Jan-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/132,118
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T95-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2013
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-758-003-1

Alignment Scores:
Pred. No.: 0 Length: 2016
Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-981-397a-16 (1-671) x US-09-758-003-1 (1-2016)

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RESULT 2

US-09-981-397A-15
 : Sequence 15, Application US/09981397A
 : Publication No. US20030082519A1
 : GENERAL INFORMATION:
 : APPLICANT: Axxima Pharmaceuticals AG
 : APPLICANT: Schubert, Daniel
 : APPLICANT: Habenberger, Peter
 : APPLICANT: Stein-Cerlach, Matthias
 : APPLICANT: Berec, Dorian
 : TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
 : FILE OF INVENTION: Inhibition
 : FILE REFERENCE: AXM-004.1 US
 : CURRENT APPLICATION NUMBER: US/09/981.397A
 : PRIOR FILING DATE: 2002-06-28
 : PRIOR APPLICATION NUMBER: 60/240,750
 : NUMBER OF SEQ ID NOS: 22
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 15
 : LENGTH: 2617
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (2141)..(2141)
 : OTHER INFORMATION: n = a,c,g or t
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (2311)..(2311)
 : OTHER INFORMATION: n = a,c,g or t
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (2452)..(2452)
 : OTHER INFORMATION: n = a,c,g or t
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (2496)..(2496)
 : OTHER INFORMATION: n = a,c,g or t
 : US-09-981-397A-15

Alignment Scores:

Pred. No.: 0
 Score: 3545.00
 Percent Similarity: 100.008
 Best Local Similarity: 100.008
 Query Match: 100.008
 DB: 9

Length: 2617
 Matches: 671
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-981-397A-16 (1-671) x US-09-981-397A-15 (1-2617)
 QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
 |||||||
 Db 1 ATGCACCCAGACAGATGCTCTGAAATGATTAAGATGAATTCACATGCTCTCGAGAGT 60
 |||||||
 QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisAspTrpGlnGly 40
 |||||||
 Db 61 GCAGAACTGCACACCGGAGGCTTTGGAGAGTGTCTGTGTGTTCCACAGACCCAGGGA 120
 |||||||
 QY 41 LeuMetIleLeuLysTrpValTrpLysGlyProAsnCysIleGluHisAsnGluAlaLeu 60
 |||||||
 Db 121 CTCATGATCATGAAGAACAGTGTACAGAGGGGCCAATTCATTTGAGCACAAGAGCCCTC 180
 |||||||
 QY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuGly 80
 |||||||
 Db 181 TTGGAGAGGCGGAAGATGATCAACAGCATGAGACACAGCCGGGTGGAGATCTCTCGGC 240
 |||||||
 QY 81 ValIleIleGluGluGlyLysTrpSerLeuValMetGluTrpMetGluLysGlyAsnLeu 100
 |||||||
 Db 241 GTCATCATAGAGAGGAGGAGTACTCCCTGGTATGAGATCATGAGAGGAGGCACTGTG 300
 |||||||
 QY 101 MethHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
 |||||||
 Db 301 ATGCACGTCGTGAAGCCGAGATGATGATCTCGCTTCTGTAAAGAGAGATATTTTG 360
 |||||||
 QY 121 GluIleIleGluGlyMetCysTrpLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
 |||||||
 Db 361 GAAATCATTTGAGAGAAATGCTACTCATGCAAAAGCGCGATACACAGAGACCTGAG 420
 |||||||
 QY 141 ProGluHisLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
 |||||||
 Db 421 CCTGAATAATCCCTGTGTGATTAATGACTTCCACTTAATGATGCGAGACTCGGCTTGCC 480
 |||||||
 QY 161 SerPheLysMetTrpSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
 |||||||
 Db 481 TCCTTTAAGATGTGAGCAAACTGAATATGAAGACATGATGAGGAGAGTGGAC 540
 |||||||
 QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTrpTrpMetAlaProGluHisLeuAsnAsp 200
 |||||||
 Db 541 GGCACCCCTAAGAAAGATGGCGGACCCCTACTACTACATGGCGCCGAGACCTGAATGAC 600
 |||||||
 QY 201 ValAsnAlaLysProThrGluLysSerAspValLysSerPheAlaValIleLeuTrpAla 220
 |||||||
 Db 601 GTCAACCCAAAGCCCAAGAGAAAGTGGATGTATGAGCTTGTGTATGATCTTGCGGC 660
 |||||||
 QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGlnLeuIleMetCys 240
 |||||||
 Db 661 ATATTTCGAATTAAGAGCCCATATGAATATCTATCTGTGAGCAGAGTGTATATGTGC 720
 |||||||
 QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTrpCysProArgGluIle 260
 |||||||
 Db 721 ATAAATCTGGGAGACAGCCAGATGCTGATGACATCACTGATGCTGCCCAAGAAAT 780
 |||||||
 QY 261 IleSerLeuMetLysLeuGlyTrpGluAlaAsnProGluAlaArgProThrPheProGly 280
 |||||||
 Db 781 ATCAGTCTCATGAAGCTCTGCTGGGAGCCGATCCGAGAGCTGCGCCGACATTTCTGCGC 840
 |||||||
 QY 281 IleGluGluLysPheArgProPheTrpLeuSerGlnLeuGluGluSerValGluGluAsp 300
 |||||||
 Db 841 ATTGAAGAAAAATTTAGGCTTTTATTTAATTAATTAAGAGAAAGTGTAGAGAGAGC 900
 |||||||
 QY 301 ValLysSerLeuLysLysGluTrpSerAsnGluAsnAlaValValLysArgMetGlnSer 320
 |||||||
 Db 901 GTGAAGAGTTTAAAGAAAGAGTATTCAACGAAAAATGCAGTTGTGAAGAGATCACTCT 960
 |||||||
 QY 321 LeuGlnLeuAspCysValAlaIleValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
 |||||||
 Db 961 CTTCACCTTATTTGTGGAGTACCTTCAAGCCGCGTCAATTAAGCCACAGAACACCTT 1020
 |||||||
 QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla 360
 |||||||
 Db 1021 GGTTCACCTGCACAGTTCACAGGAGACTTGGATGGGTCTCTGTGAGAGAGTCTCTGTTGCT 1080
 |||||||

```
QY 361 ProSerLeuGluHisProGlnGluHisGlnProSerLeuGlnSerLysLeuGlnAsp 380
DB 1081 CTTTCCCTGGAGCACCACAGAGAGAAAGAGCCAGCCTGACAGATTAATCAACCAAGAC 1140
QY 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
DB 1141 GAAGCCACTACATCTTTATGCGACCGCATGAGACAGACAGCAAGCAAGCCACCA 1200
QY 401 GlnAsnValAlaLysAsnArgGluGluGluValArgArgValSerHisAspProPhe 420
DB 1201 CAGAAATGGCTTACACAGAGAGAGAGAAAGAGACGACGAGCTCCCATGACCTTTT 1260
QY 421 AlaGlnGlnArgProTyrGlnAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer 440
DB 1261 GCACAGCAAGACCTTACAGAGATTTTCAGAAATACAGAGAGAAAGACCTGTTATTC 1320
QY 441 SerAlaAlaSerHisGlnValAlaHisGlnProSerGlyLeuThrSerGlnProGln 460
DB 1321 AGTGCAGCCAGTCATGTAATGACAGCCAGCCCTCAGGCTCAGCCAGCCACCTCA 1380
QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
DB 1381 GTACTGTATCAGAACATGATTAATATGCTCATGCTGCTTGGACACAGACCTGGAT 1440
QY 481 ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
DB 1441 CCAGAGACGACGAGTCCAGAGTTGCTGACAGCCCAATTCAGATCATGCTAGTCTG 1500
QY 501 HisAsnIleProValProGlnThrAsnTyrLeuGlyAsnThrProThrMetProPheSer 520
DB 1501 CATTAATATCCAGTGCCTGAGACCAACTCATAGGAATATCACCCACCTGCTTAC 1560
QY 521 SerLeuProProThrAspGlnSerLysTyrThrIleTyrAsnSerThrGlyIleGln 540
DB 1561 TCCTTGCACCAACAGATGAATCTATAAATATACATATACAAATAGTCTGCAATTC 1620
QY 541 IleGlyAlaTyrAsnTyrMetGlnIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
DB 1621 ATTGAGGCTTACAAATTAATGAGATGGTGGAGAGTTCATCACTACTATACAGACACA 1680
QY 561 AsnThrAsnPheLysGluGlnProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
DB 1681 AATAGCAACTTCAAGAGAGAGCCAGCTGCTAGTACCAAGCATCTTGTATATATCCACT 1740
QY 581 SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTrrPlysAsn 600
DB 1741 AGTCTGACGAGATAAACACCTGAGCCCAATCAGGGAAATCTGGAAAGACACTGAA 1800
QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGlnIleAspHisAspTyrGlu 620
DB 1801 TGTGCCCTTAAACTGGCTTACACAGTCTCAGATTGATGAATGACCATCATCATATAG 1860
QY 621 ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTrrValMetArgGluGly 640
DB 1861 CGAGATGAGACTGAAAGAAAGATTACAGATGCTCCAAAGTGGCTGATAGGGAAGGC 1920
QY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
DB 1921 ATTAAGGAGGAGCCAGGTGGGAGAGTGGCCAGGCGCTCCACAGTGTTCAGAGATC 1980
QY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
DB 1981 CTTCAGACGCTGATTTACGTACAGCCAGAAC 2013
```

RESULT 3

```
US-09-854-133-676
: Sequence 676, Application US/09854133
: Publication No. US20020183499A1
: GENERAL INFORMATION:
: APPLICANT: Lohes, Michael J.
: APPLICANT: Mohamath, Radooh
: APPLICANT: Henderson, Robert A.
```

```
: APPLICANT: Benson, Darin R.
: APPLICANT: Secrist, Heather
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
: TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.475C10
: CURRENT APPLICATION NUMBER: US/09/854,133
: NUMBER OF SEQ ID NOS: 735
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 676
: LENGTH: 529
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-854-133-676
```

Alignment Scores:

Pred. No.:	1,14e-69	Length:	529
Score:	772.00	Matches:	169
Percent Similarity:	95.48%	Conservative:	0
Best Local Similarity:	95.48%	Mismatches:	5
Query Match:	21.78%	Indels:	6
DB:	9	Gaps:	0

US-09-981-397a-16 (1-671) x US-09-854-133-676 (1-529)

```
QY 274 AlaArgProThrPheProGlyIleGluGluLysPheArgProPheTyrLeuSerGlnLeu 293
DB 8 GCACGAGGACACATTTCTGCTGCAATGAGAAAATTTAGCCCTTTTATTAATGTCATATA 67
QY 294 GluGluSerValGluGluAspValLysSerLeuLysGlyLysTyrSerAsnGlu-AsnAl 313
DB 68 GAGAAAGTGTAGAGAGAGAGAGCTGAAGAGTTTAAAGAAAGATTAATCAACGAAAAATGC 127
QY 313 aValValLysArgMetGlnSerLeuGlnLeuAspGlyValAlaValProSerSerArgSe 333
DB 128 AGTTGTGAGAGAAATGACATCTCTTCA-CTTGATTTGTGGCAGTCACTTCAMCCGGTTC 186
QY 333 rAsnSerAlaThrGlnGlnProGlySer-LeuHisSerSerGlnIleGluGlyMetGlyP 353
DB 187 AATTCAGGCACAGAAAGAGCCGTGTTCACTTCCACAGTTCCTCCAGGAGACTTGGATGGGTC 246
QY 353 rValGluGluSerTrrPheAlaProSerLeuGlnHisProGlnGluGluAsnGluProS 373
DB 247 CTGTGAGAGAGTCTGCTGCTTCCCTGAGCACCCACCAAGAAAGATGAGCCCA 306
QY 373 erLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspA 393
DB 307 GCCTCAGAGTAACCTCCAGAGCAAGCCAC-TACCATCTTTATGCGACGCGCATGAGACA 365
QY 393 rGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArgGluGluGluArgArgA 413
DB 366 GCGACAGCAAGACAGCAGCCAGACAGATGTGGCTTACACAGAGAGAGAGAAAGAGAC 425
QY 413 rGArgValSerHisAspProPheAlaGlnGlnArgProTyrGlu-AsnPheGlnAsnThr 432
DB 426 GCAGGCTCCCATGAGACCTTTTGACACAGCAAGACCTTTAGAGAAATTTTCAGAAATACA 485
QY 433 GluGlyLysGlyThrValTyrSerSerAlaHisSerHisGlyAsn 447
DB 486 GAGGAGAAAGGCTGTGT-TATTCAGTGTGACAGCCAGTCAATGTGTAAT 529
```

RESULT 4

```
US-09-918-995-17425
: Sequence 17425, Application US/09918995
: Publication No. US20030073623A1
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
: FILE REFERENCE: 20411-756
: CURRENT APPLICATION NUMBER: US/09/918,995
: CURRENT FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: US/09/235,076
```

```
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17425
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-17425

Alignment Scores:
Pred. No.: 176-56 Length: 392
Score: 641.00 Matches: 125
Percent Similarity: 96.92% Conservative: 1
Best Local Similarity: 96.15% Mismatches: 4
Query Match: 18.08% Indels: 0
DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x US-09-918-995-17425 (1-392)

QY 292 GlnleuglucjuserValGluGluaspValysSerleuLysGluTyrSerasnGlu 311
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1 CAATTAGAGAGAAAGGATATAGAGACGTGAGTTTAAAGAAAGATATTCAACGAA 60

QY 312 AsnaIaValIyLysArgmetGlnSerleuGlnleuaspCyValAlaValProSerSer 331
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 61 AATCAGCTTGTGAAGAGAAATGCACTCTTCACTTGATGTGGGGCAGTACCTTCAAGC 120

QY 332 ArgserasnSerAlaThrGlnGlnProGlySerleuHisSerSerGlnGlyLeuGlyMet 351
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 121 CGGCAAAATTCAGCCACAGAACACCTGGTCACTGCACACTGCCAGGAGCACTGGGATG 180

QY 352 GlyProValGluGluSerTyrPheAlaProSerleuGlnHisProGlnGluGluasnGlu 371
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 181 GGTCCTGTGGAGAGTCTCTGTTGCTTCCTCGAGCAGCCACAGAAAGAGAAATGAG 240

QY 372 ProSerleuGlnSerLysleuGlnAspGluAlaasnTyrHisleuTyrGlySerArgMet 391
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 241 CCCAGCCTGCAGATAACTCCAGACGAAACCAACTCATCTTTATGCGAGCGCATG 300

QY 392 AspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArgGluGluArg 411
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 301 GACAGGAGAGAGAAACAGACGCCACAGAGATGTGCTTACACAGAAAGAGGAAAG 360

QY 412 ArgArgValSerHisAspProPheAla 421
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 361 AGAGCGAGGAGTCTCCATGACCTTTTGCA 390

RESULT 5
US-09-796-692-6140/c
; Sequence 6140, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077 001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
```

```
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6140
; LENGTH: 331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-6140

Alignment Scores:
Pred. No.: 431e-46 Length: 331
Score: 538.00 Matches: 102
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.18% Indels: 0
DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x US-09-796-692-6140 (1-331)

QY 570 AlayrTyrGlnAlaIlePheaspAsnThrSerleuThrAspLysHisleuaspPro 589
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 329 GCTAGATGCCAAGCATATCTTGTGATAATATACACTAGTGTGAGCGATTAACACTGGACCCA 270

QY 590 IleArgGluAsnLeuGlyLysHisTyrLysAsnCySalaArgLysLeuGlyPheThrGln 609
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 269 ATCAGGGAAATCTGGGAAACACTGGAATAAATCTGCCCTAAACTGGCTTCACACAG 210

QY 610 SerGlnIleAspGluIleAspHisAspTyrGluArgAspGlyLeuLysGluLysValTyr 629
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 209 TCTCAGATTGATGAATGACCATGACTATGAGGAGTGGAGTGAAGAAGAGGTTTAC 150

QY 630 GlnMetLeuGlnLysTyrValMetArgGluGlyLysGlyAlaThrValGlyLysLeu 649
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 149 CAGATGCTCCAAAGTGGGTGATGAGGAGCAATAAAGGAGCCAGCGTGGGAGCTG 90

QY 650 AlaGlnAlaLeuHisGlnCysSerArgIleAspLeuLeuSerSerleuIleTyrValSer 669
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 89 GCCCAGGCGCTCCACACAGTGTCCAGATGACCTTGCAGCAGCTGATTTACGTACGC 30

QY 670 GlnAsn 671
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 29 CAGAAC 24

RESULT 6
US-10-040-862-6140/c
; Sequence 6140, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
```

```

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6140
; LENGTH: 331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-6140

Alignment Scores:
Pred. No.: 4 31e-46 Length: 331
Score: 538.00 Matches: 102
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.18% Indels: 0
DB: 9 Gaps: 0

US-09-981-397a-16 (1-671) x US-10-040-862-6140 (1-331)
QY 570 AAlaATYRGlnAlaAllePheAspAsnThrThrSerLeuThrAspLysHisLeuAspPro 589
DB 329 GCTAGTACCAAGCATATCTTTGATATATACCACTAGCTGACGATTAACACCTGACCCCA 270
QY 590 lIeaTgLuAsnLeuGlyLysHisTrpLysAsnCysAlaArGlyLsLeuGlyPheThrGln 609
DB 269 ATCAGGAGAAATCTGGGAAGCACATGGAAGAACTGCCCCGTAACCTGGGCTTCACACAG 210
QY 610 SerGlnIleAspGluIleAspHisAspTyrGluArGAspGlyLeuLysGluLysValTyr 629
DB 209 TCTCAGATTGATGAATGATGACCATGACATGAGCGAGATGCGACTGAAAGAAAGGCTTAC 150
QY 630 GlnMetLeuGlnLysTrpValMetArgGluGlyIleLysGlyAlaThrValGlyLysLeu 649
DB 149 CAGATGCTCCCAAAAGTGGGTATGAGGAGCAATAAAGGAGCCAGGTGGGAGAGCTG 90
QY 650 AlaglnAlaLeuHisGlnCysSerArgIleAspLeuLeuSerSerLeuIleTyrValSer 669
DB 89 GCGCCAGCGCTCCACACAGTGTCCAGATCGACCTTCGAGAGCTTGTATTACGTCAGC 30
QY 670 GlnAsn 671
DB 29 CAGAAC 24

RESULT 7
US-09-879-536-495
; Sequence 495, Application US/09879536
; Patent No. US20020144298A1
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
```

```

; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dertl, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/879,536
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/088,801
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 495
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(606)
; OTHER INFORMATION: n = A,T,C or G
US-09-879-536-495

Alignment Scores:
Pred. No.: 5 71e-44 Length: 606
Score: 521.00 Matches: 99
Percent Similarity: 99.00% Conservative: 0
Best Local Similarity: 99.00% Mismatches: 1
Query Match: 14.70% Indels: 0
DB: 10 Gaps: 0

US-09-981-397a-16 (1-671) x US-09-879-536-495 (1-606)
QY 572 TyrGlnAlaAllePheAspAsnThrThrSerLeuThrAspLysHisLeuAspProIleArg 591
DB 3 TACCAAGCATATCTTTGATATATACCACTAGCTGACGAGTAAACACCTGACCCATCAGC 62
QY 592 GlnAsnLeuGlyLysHisTrpLysAsnCysAlaArGlyLsLeuGlyPheThrGlnSerGln 611
DB 63 GAAATCTGGGAAACACATCGAAGAAACTGCCCCGTAACCTGGGCTTCACACAGCTCAG 122
QY 612 lIeaSpGluIleAspHisAspTyrGluArGAspGlyLeuLysGluLysValTyrGlnMet 631
DB 123 ATTGATGAATTTGACCATGACTATGAGCGAGATGAGTGAAGAAAGGATTTACCGAGATG 182
QY 632 LeuGlnLysTrpValMetArgGluGlyIleLysGlyAlaThrValGlyLysLeuAlaGln 651
DB 183 CTCCAAAAGTGGGTATGAGGAGCAATAAAGGAGCCAGCGTGGGAGAGCTGGCCAG 242
QY 652 AlAlaLeuHisGlnCysSerArgIleAspLeuLeuSerSerLeuIleTyrValSerGlnAsn 671
DB 243 GCGCTCCACACAGTGTCTTGATCGACCTTCGACACAGCTTGATTACGTACGCCAGAAC 302

RESULT 8
US-09-960-352-4340
; Sequence 4340, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nenping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4340
; LENGTH: 430
```

TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 19-LIB3057-015-Q1-K1-E11
US-09-960-352-4340

Alignment Scores:

Pred. No.:	2.86e-38	Length:	430
Score:	463.00	Matches:	92
Percent Similarity:	71.72%	Conservative:	12
Best Local Similarity:	63.45%	Mismatches:	39
Query Match:	13.06%	Indels:	2
DB:	10	Gaps:	1.

US-09-981-397a-16 (1-671) x US-09-960-352-4340 (1-430)

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OY 423 GlnAlpProThrgluAsnPhnGlnAsnThrlGluGlyLysGlyThrValTyrSerSerAla 442
DB 1 CAGAGACCTTATGAGTCTGCTCAGAGCCAGGATTAAGCCCTGCTTACCTGCTGCTG 60
OY 443 AlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeu 462
DB 61 ATGAGTCAACACAGTGCAGCCAGACCCAGCGGGCTTAAGCAACCCCACTACCA 120
OY 463 TyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGly 482
DB 121 TACTGGAGAGATGGA-----TCATTTCATCCGCTTGAGTGAAGCCGCTGAGCTGGG 174
OY 483 ThrAlaGlyProAlaValTyrPyrArgProIleProSerHisMetProSerLeuHisAsn 502
DB 175 ACATGACGTCCACAGAGTTTGATGGCCAAACCCAGCCACGACATGCTGTATAAA 234
OY 503 IleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeu 522
DB 235 ACATGACGTCCGAGAGCTGCTGCTGGAACACACACCATTCATTCACCTCTTG 294
OY 523 ProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIleGly 542
DB 295 CCATCAAGAGATGATGCTTCAAAATATACCATACACAGCATGCTGCTGATTCAGATTGGC 354
OY 543 AlaTyrAsnTyrMetGluIleGlyIleThrSerSerSerLeuLeuAspSerThrAsnThr 562
DB 355 GACAGTATTAATCAATGAGATTGGTGAATGATTCATGCTGCTGACACACATACATG 414
OY 563 AsnPhelysGluGlu 567
DB 415 AACCTGAAGAAGAG 429
```

RESULT 9

US-10-198-846-13921

Sequence 13921, Application US/10198846

Publication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steilmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198, 846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ. ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13921

LENGTH: 2111

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931,

LOCATION: 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941,
LOCATION: 1942, 1943, 1944, 1945, 1946, 1947, 1948, 2007, 2096, 2110,
LOCATION: 2111
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13921

Alignment Scores:

Pred. No.:	1.83e-35	Length:	2111
Score:	445.50	Matches:	152
Percent Similarity:	42.59%	Conservative:	101
Best Local Similarity:	25.59%	Mismatches:	187
Query Match:	12.57%	Indels:	155
DB:	9	Gaps:	22

US-09-981-397a-16 (1-671) x US-10-198-846-13921 (1-2111)

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OY 1 MetGlnProAspMetSerLeuAsnValIleLys----- 11
DB 156 CTGCACACCTTCCAGCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 215
OY 12 MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyGlyPheGlyLys 30
DB 216 TTGGTGTTCATCGAGAGCTGAGAACAGGAGCTGCTGGCAAAAGCGGGTTCGGACAA 275
OY 31 ValSerLeuGlySerPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50
DB 276 GTGTTCCGGCGGCACATAGGAAGTGGGC-----TACGATGTG 314
OY 51 ProAsnGlyIleGluHisAsnGluAlaLeuGluGluAlaLysMetMetAsnArgLeu 70
DB 315 GCGGTCAAGATCGTAACCTGGAAGCGATATCCAGGAGGTCAAGGCCCATGCGCAAGCTG 374
OY 71 ArgHisSerArgValValLysLeuLeuGlyValIle-----IleGluGlu 85
DB 375 GATTAACGAATTCGCTGCGCTGAGAGGGATTATCCAGAGGTGAACGTAACGACCAAGAT 434
OY 86 GlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLys 105
DB 435 CCCAAGCCGGCTCGTGAGTACTAATTCATGAGAACGGCTCTTGCGGGGCTGCTGAC 494
OY 106 AlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeuGluIleIleGluGly 125
DB 495 TCCACAGTCCCTGCGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 554
OY 126 MetCysTyrLeuHisGlyLysGly-----ValIleHisLysAspLeuLysProGluAsn 143
DB 555 ATGTTTACTCTGACGACGACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
OY 144 IleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLys 163
DB 615 GTCTCTGTGACCCACAGAGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACG 674
OY 164 MetTyrSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAspGlyThrAla 183
DB 675 GGAAGCTCACAG-----TCAGGGACAGCG 658
OY 184 Lys---LysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAsn 202
DB 699 TCCGGGAGGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 758
OY 203 AlaLysProThrGluLysSerAspValTyrSerPheAlaValLeuTyrPalaIlePhe 222
DB 759 CGAAGGCTTCACACAGCACTGACGTACAGCTGCGGATCTCAATGCTGCGCAGTCTT 818
OY 223 AlaAsnLysGlu-----ProTyrGlu-----AsnAlaIleCysGlu 234
DB 819 GCTGAGAGAGAGATTGAGTTGCCAACGACCAATCACTGCTGACAGCAGTGTCAAC 878
OY 235 GlnGlnLeuIleMetCysIleLysSerGlyAsnArgProAspValAspPheIleThrGlu 254
DB 879 AGGCAG-----ACCGGCTTCATGCTGAGTGGCCCA 914
OY 255 TyrCysProArgGlu-----IleIleSerLeuMetLysLeuGlyTyrGlu 269
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Db	915	GCCGGCGCTGAGACTCCGCGCTTGAAGAGCACTGAGAGAGCTAATGACTTCGTCGGAGC	974
Oy	270	AlaasnProgluAlaargProthPhe-----ProglylleGlulysPhe	285
Db	975	AGTGAGCCCAAGAGACAGACCTCTCTCCAGGAATGCCAACAAAACGTGATCAACTCTTC	1034
Oy	286	ArgProPheTyLeuSerGlnLeuGluservAlaGluLysaspVallysSerLeuIys	305
Db	1035	CAG-----ATGGTGAGAACATATGATGCTGCTGCTCCAGCGTAAG	1079
Oy	306	LysGluTySerasnGluasnAlaValIalysargMetGlnSerLeuGlnLeuaspCys	325
Db	1080	GATTTCTCTGCTCAGCTCAGAGCAGCAATGAGCATTT-----	1118
Oy	326	ValAlaValProSerSerArgSerasnSerAlaThrGluGlnProGlySerLeuHisser	345
Db	1119	---TCTATCCCAAGACTCA-----	1133
Oy	346	SerGlnGlyLeuGlyMetGlyProValGlnLusertTrpPheAlaProSerLeuLHis	365
Db	1134	-----GGCCAGAGAGGAGACAAATAGTGAGCTTTAGAGAACCATACAAAC	1181
Oy	366	ProGlnGluGluasnGlnProSerLeuGlnSerIysLeuGlnAspLalaasnTyHis	385
Db	1182	CAGCACTCTCATATGATGATGATGTTCTGAGTGGCTA-----	1220
Oy	386	LeuTyrglySerArgMetAspArgGlnThrIysGlnGlnProAlaGlnAsnValAlaTyrr	405
Db	1221	-----AACAAATCTGATCTAGAGGAGCCTCCAGCTGTGT-----	1255
Oy	406	AsnArgGluGluGluArgArgArgValSerHisAspProPheAlaGlnIlnArgPro	425
Db	1257	-----CCTAA-AAATGCCGAGGCT	1276
Oy	426	TyrgluAsnProGlnAsnThrGluGlyLysGlyThrValIyrrSer-SerAlaAlaSerHi	445
Db	1277	TACCAAGAGGAGCAGGGCCACAGAGAGACAGATTTCCACAAAGCTGGACAGGACATC	1338
Oy	445	sglyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrglnAs	465
Db	1337	TTTCAGATTCCATGGCCCAACT-----CCCAGACTCCAGAGACCTCAACTTTAG	1387
Oy	465	nasnGlyLeuTyrrSerSerHisGlyThrArgProLeuAspProGlyThrAlaGln	485
Db	1388	AAACCAGATGCCCAAGC-----CCTACCTCAATGGAGACA-----	1421
Oy	485	yProArgValIrrTyrrArgProLleProSerHisMetProSerLeuHisAsnIleProva	505
Db	1422	-----CCAAAGT-----CCTGG	1433
Oy	505	LProGluThrAsnTyrrLeuGlyAsnThrProThrMetProPheSerSerLeuProProTh	525
Db	1433	ACCCGAGGGAATCAGGGGCTGAGAGACAAAGCATGACATGCTCTCCAGAGCCCCGA	1493
Oy	525	raspGluSerIleIys-----TyrrThrLleTyrrasnSerThrGlylleGlnI	541
Db	1493	GCCAAATTCATACAGAGGCGACCGCTCGTTAAACATATACAACTGCTGTGGGTCGAAGT	1552
Oy	541	eglyAlaTyrrasnTyrrMetGluIleGlyGlyThrSerSer	554
Db	1553	TGGAGACACAACTTACTTACTTACCAACAGACAACTGCC	1592

RESULT 10
US-09-862-027-7
Sequence 7, Application US/09862027
Patent No. US200201428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. US00201428A1el Kinases and Uses Thereof
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21

```

US-09-981-397A-16 (1-671) x US-09-862-027-7 (1-1697)

PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1697
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2)...(1492)
US-09-862-027-7

Alignment Scores:
Pred. No.:      4,82e-35      Length:      1697
Score:          440.00      Matches:      148
Percent Similarity: 42.86%      Conservative: 95
Best Local Similarity: 26.10%      Mismatches:  179
Query Match:    12.41%      Indels:      146
DB:            10      Gaps:        21

```

QY 19 GIsSerAlaGluIuLeu---AspSerGlyGlyPheGlyValSerLeuGlyPheHisArg 37
 |||::: ||||| ||| ||||| ||||| ||| ||||| |||
 Db 2 GAGACACAGAGAGCTCGCGCAAGGCGGGTTCGCACAGTGTTCGGGCGCAACATAG 61
 QY 38 ThrGlnGlyLeuMetIleMetLysThrValTyrGlyProAsnGlyIleGlnHisAsn 57
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 62 AAGTGGGCG-----TAGAGTGGCGGTCAACATCTTAACATCG 10
 QY 58 GlnAlaLeuLeuGlnGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLys 77
 ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 101 AAGCGCATTCAGGAGAGGTCAAGGCCATGGCAAGTGTGAATACCAATTCCTGGCGCC 16
 QY 78 LeuLeuGlyValIle-----IleGlnGlyLysThrSerLeuValMet 92
 ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 161 CTGAAGAGGGTTTCTCCAGAAGGTGAACTGGGACCAAGATCCCAAGCGGCTGTGTGACT 22
 QY 93 GluTyrMetGlnLysGlyAsnLeuMetHisValLeuLysAlaGluMetSerThrProLeu 11
 ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 221 AAATTCATGAGAAAGCGCTCTGTGGGGCTCTGCAGTCCCAAGGCCCTGGCGCTGG 28
 QY 113 SerValLysGlyArgIleLeuGlnIleIleGlnGlyMetCysTyrLeuHisGlyLys 13
 ::::: ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 281 CCGCTCTCTTGGCCGCTGTGAAGAAGGTGTGGATGTCTTACCTGCAGACAGCAG 34
 QY 133 Gly-----ValIleHisLysAspLeuLysProGlnAsnIleLeuValAspAsnSph 15
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 341 AACCCGGTGTCTCTGCACCGCGACCTCAAGCCATTCACAGCTCTGTGCACCAAGCTG 40
 QY 151 HisIleLysIleAlaAspLeuGlyLeuAlaSerPheLysMetArgPserLysLeuAsn 17
 |||::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 401 CACGTCAAGTGGCAGATTTTGGCTGTCCACATTTCAAGGAGGCTCAGACAG----- 45
 QY 171 GlnGlnHisAsnGluLeuArgGlnValAspGlyThrAlaLys---LysAsnGlyLysThr 18
 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 452 -----TCAGGAGACAGGGTCCGGGAGCGCAAGGCGGCAAC 48
 QY 190 LeuTyrTyrMetAlaProGlnHisLeuAsnAspValAsnAlaLysProThrGluLysSer 20
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 485 CTGGGCTACTTGGCCCCAGACACTGTTGTTAACGTAAACCGGAAGGCCCTCCACAGCCAGT 54
 QY 210 AspValTyrSerPheAlaValValLeuTyrPalaIlePheAlaAsnLysGlu----- 22
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 545 GACGCTACAGCTTCGGGATCCCAATAGTGGGAGTCTTGTGGGAAGAAAGTTAGTTGG 60
 QY 227 ProTyrGlu-----AsnAlaIleCysGlnGlnGlnLeuIleMetCysIle 24
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 605 CCAACCGAACCATCACTCGTGTACGAAAGCAGTGTGAACAGGACAG----- 64
 QY 242 LysSerGlyAsnArgProAspValAspAspIleThrGlnTyrCysProArgGlu----- 25

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Db 650 -----AACGGGCTTATTGGCTGACCTGCCCCAACCGGGGCTGAGACTCCGGC 700
QY 260 -----lleleSerleuMetLysLeuCystrpGluAlaasnProgluAlaargPro 276
Db 701 TTGAGAGAGACTGAAGAGGATGACGCTGCTGGAGCAGTGAAGCCCAAGAGACAGACC 760
QY 277 ThrPhe-----ProGlylleGluGlnLysPheargProPheTYrLeuSerGln 292
Db 761 TCCCTCCAGGAATGCCCTACCAAAAACGATGAAGTCTTCCAG-----ATG 805
QY 293 leuGluGlnSerValGluGlnAspValLysSerleuLysLysGluTYrSerAsnGluasn 312
Db 806 GTGGAGACAAATATGAATGCTGCTGTCCACGGTAAGATTCTCTCTCAGCTCAGC 865
QY 313 AlavalValLysArgMetGlnSerleuGlnLeuaspLysValAlaValProSerSerArg 332
Db 866 AGCAGCAATGAGAGATT-----TCTATCCAGAGTCA--- 898
QY 333 SerAsnSerAlaThrGlnGlnProGlySerleuHisSerSerGlnGlyLeuGlyMetGly 352
Db 899 -----GGCCAAAGA 907
QY 353 ProValGluGlnSerTrpPheAlaProSerleuGlnHisProGlnGlnGluAsnGluPro 372
Db 908 GGGACAGAAATGGAATGCTTTAGCAGAACCATAGAAAACAGACACTCTCTAATGATGTC 967
QY 373 SerleuGlnSerLysLeuGlnAspGluAlaAsnTYrHisleuTYrGlySerArgMetAsp 392
Db 968 ATGGTTTCTGAGTGGCA-----AAC 988
QY 393 ArgGlnThrLysGlnGlnProArgGlnAsnValAlaTYrAsnArgGluGlnGluArg 412
Db 989 AAACGTCAATGATAGAGGCTCCAGCTCTGT----- 1021
QY 413 ArgArgValSerHisAspProPheAlaGlnGlnArgProTYrGluAsnProGlnAsnThr 432
Db 1022 -----CCTAA-AAATGCCCGAGCTTACCAAGAGGAGCAGGCGACA 1062
QY 433 GluGlyLysGlyThrValTYrSer-SerAlaAlaSerHisGlyAsnAlaValHisGlnPro 452
Db 1063 AGAGAGACAGGCTTCCACACCGCTGGACAGCAGCAGCATCTTCAGATTGCGTCCACACC 1122
QY 452 oSerGlyLeuThrSerGlnProGlnValLeuTYrGlnAsnAsnGlyLeuTYrSerSerHis 472
Db 1123 T-----CCCCAGACTCCAGACCTCAACTTTCAGAAACAGATGCCACAC----- 1168
QY 472 sGlyPheGlyTYrArgProLeuAspProGlyThrAlaGlyProArgValTrpTYrArgPro 492
Db 1169 -----CCTACCTCAACTGGAACA----- 1186
QY 492 oileProSerHisMetProSerleuHisAsnIleProValProGluThrAsnTYrLeuGln 512
Db 1187 -----CCAGT-----CTGGAGCCCCGAGGGAATCAGGGGGC 1218
QY 512 yAsnThrProThrMetProPheSerSerleuProProThrAspLysSerleuLys----- 530
Db 1219 TGAGAGACAGAGCATGATGCTCTCCAGACCCCGGAGCAAAATCCAGTAACAGGGCG 1278
QY 531 -----TYrThrIleLysAsnSerHisGlyIleGlnIleGlyAlaTYrAsnTYrMetGln 548
Db 1279 ACCGCTCGTTACATATACAAATGCTCTGGGTGCAAGTGGAGACAAACAATCTTAC 1338
QY 548 uileGlyGlyThrSerSer 554
Db 1339 TATGCAACAGACAACTGCC 1357

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RESULT 11
US-10-164-080-1

; Sequence 1, Application US/10164080
; Publication No. US20030087411A1
; GENERAL INFORMATION:
; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, M.

```

; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR) AND
; TITLE OF INVENTION: USE
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(2367)
; OTHER INFORMATION:
US-10-164-080-1

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Alignment Scores:
Pred. No.: 8.09e-32 Length: 2370
Score: 410.50 Matches: 164
Percent Similarity: 43.43% Conservative: 84
Best Local Similarity: 28.72% Mismatches: 209
Query Match: 11.58% Indels: 116
Gaps: 25

```

US-09-981-397a-16 (1-671) x US-10-164-080-1 (1-2370)

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QY 14 SerSerAspPheLeuGlnSerAlaGlnLeuAspSerLysGlyPheGlyValSerLeu 33
Db 64 GCCGCGAATTCGAGGCTGGAGAGAGTGCGGCGGCTCCGCGGAGGCTACAG 123
QY 34 CysPheHisArgThrGlnGlyLeuMetIleMetLysThr-----ValTYrLysGly 50
Db 124 GTGGCGCAT-----GTGCATGGAAGACGTGGCTCCGATCAAGTCTCG 168
QY 51 ProAsnCyS-----IleGlnHisAsnGlu-----AlaLeuGlnGluAlaLysMetMet 67
Db 169 CCCAGTCTGCACGTCGACAGCAGAGAGAGATGAGAGCTCTGGAGAACTAAGAGATG 228
QY 68 AsnArgLeuArgHisSerArgValValLysLeuLeuGlnValIleIleGluGluGlyLys 87
Db 229 GAGATGGCCAAAGTCCGATACATTCTACCTGTACCGCATATGCCAGAA-----CCT 282
QY 88 TYrSerLeuValMetGluTYrMetGluGlyAsnLeuMetHisValLeuLysAlaGlu 107
Db 283 GTGGCTTGGTCATGAGGATGATGACAGACAGCTCCCTGAGAAAGCTGCTGCAGAG 342
QY 108 MetSerThrProLeuSerValLysGlyArgIleIleLeuGlnIleIleGluGlyMetCyS 127
Db 343 ---CCATTGGCTTGGAGCTGGCGCTTTCGATGTCGACAGACAGCCGAGGATGAC 399
QY 128 TYrLeuHis-----GlyLysGlyValIleHisLysAspLeuLysProGluAsnIleLeu 145
Db 400 TTCTGATTCATGATGCTCCGCCCTGCTCACCCTAGACCTGAAGCCAGGACATCTCTG 459
QY 146 ValAspAsnAspPheHisIleLysIleAlaAspLeuGlnLeuAlaSerPheLysMetTrp 165
Db 460 CTGGATCCCACTACATGTCATGATGATTTGACTTTGGCTGGGC----- 504
QY 166 SerLysLeuAsnAsnGlnGlnHisAsnGlnLeuArgIleValAspGlyThrAlaLysLys 185
Db 505 ---AAGTCAATGAGCATGTCCTCCACTCTCAGACTCAGCTGATGGCTGTT----- 555
QY 186 AsnGlyGlyThrLeuTYrTYrMetAlaProGlnHisLeuAsnAspValAsnAlaLysPro 205
Db 556 -----GTACCAATCGCTTACCTCCCTCCAGAGAGATTCGTAGAGAGACCCCTTGT 609

```

QY	206	ThrGluSerSerAspValTyrSerPheLeuAlaValLeuThrPalaIlePheHisLys	225
Db	610	GACACCAACATGATGTTACAGCTTCGCGATTGTGATGGGGTGCTTACACAGAAG	669
QY	226	GluProTyrGluAsnAlaIleCysGluGlnGlnLeuIleMetCysIleLysSerGlyAsn	245
Db	670	AAGCATTTTGGAGTAAGAAAGAACATCTGTACACATCATGATGAAGTGGTAAAGGCCAC	729
QY	246	ArgProAspValAspAspIleThrGluTyrCysProArg-----GluIleLeuSer	262
Db	730	CGCCCAAGAGCTGCCACCCATCTGGACACCCGGCGCGCTGGCTGTGCACAGCTGTATGAGG	789
QY	263	LeuMetLysLeuCysTyrPheGluAlaAsnProGluAlaArgProThrPheProGlyIleGlu	282
Db	790	CTCATATGCAACGGGTGTGGCATGTACACACCACAGTGGGGCCCATCTCCAAAGAAATTTCC	849
QY	283	GluTyrPheArgProPheTyrLeuSerGlnLeuGlnGluSerValGluAlaAspValLys	302
Db	850	TCGTGA-----ACAGAACACCTTTGTGTGAGAACGCCATGATGAGAGAGGTGAA	894
QY	303	SerLeuLysLysGluTyrSerAsnGluAsnAlaValLysArgMetGlnSerLeuGln	322
Db	895	GACCTGGCTCATGAGCCAGCGAGAAAGC-----TCTCTAAG	933
QY	323	LeuAspCysValAlaValPro---SerArgTyrSerAsnSerAlaThrGlnGlnProGly	341
Db	934	TCCAAAGATGAGGCCAGGCCGAGTCTGCACAGCTTCCAGCGCGCTGCTCCGCCCTTC	993
QY	342	SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGlnGluSerTyrPheAlaPro	361
Db	994	GATACAGACTGCAGTCTCTCCGAGTGTCTGTACAGTTG---GACTCTGGGATCTCCAG	1055
QY	362	SerLeuGlnHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeu---GlnAsp	380
Db	1051	ACTCTTGAAGGCCGCCGAGAGACTCGACGCCAAGTTCTCTGTATGACAGCTCCCATCTC	1110
QY	381	GluAlaAsnTyrHisLeuTyrGly---SerArgMetAspArgGlnThrLysGlnGlnPro	399
Db	1111	AGCATGGCAGAAAGGCTCTCGGGGGTGTCTCAGTGCAGTACAGCTTTTCTCCAGAGA	1170
QY	400	ArgGlnAsnValAlaTyrAsnArgGluGluGluAlaGlyArgArgValSerHisAspPro	419
Db	1171	TCGCTGTACAGTCTTTTGGAGCGGAGACTTC-AACAGGCCA-----CCT	1214
QY	420	PheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGlnGlyLysGlyThrValTyr	439
Db	1215	GGGCCCCACAGATCCAGAGAA-----GAAGCTAGTGATGCCATCAT	1255
QY	440	SerSerAlaIleAsnHisGlyAsnAlaValHisGlnProSer-----GlyLeu	455
Db	1260	-----ATCAGGGGACACACAGAGCGTGTATAGATCTCTACAGCCCCAAGATGTGGACTT	1313
QY	456	ThrSer-----	457
Db	1314	GGTTCCTAGACAGCACTGCCAGCTGTGCTACCTGGCTGTGAGCGCCGACAGAGAGACTG	1373
QY	458	-----GlnProGlnAlaLeuTyrGlnAsnAsnGlyLeu	468
Db	1374	TGTCAAGTGGCTGTGCTTAACTATGCCAACCCCAACT---GAACCAACAGAGAGGCTC	1430
QY	469	Tyr---SerSerHisGlyPheGlyThr-----	476
Db	1431	TACACCACTGCATATGGCTGTGGAGCGGAAAGAGAGCTGGAATGTGAGCTATGCTAGC	1490
QY	477	-----ArgProLeuAsp---ProGlyThrAlaGlyP	486
Db	1491	CCGAGAGACCACTGTCATGCCAAGAGATGAAGACCAAGTGCCTCCATTCCTGGACG	1550
QY	486	roArgValTyrTyrArgProIleProSerHisMetProSerLeuHisAsnIleProValP	506
Db	1551	CCAGATGGGATGAGGCCACACAGAGCTC-TCTCTAGAG---AAGATCTCTGTGCA	1606
QY	506	roGluThrAsnTyrLeuGlyAsnThrPro	515

Db	1607	ATGAGGTGGACTTTGAAGGCCGAAACACC	1635
		:	
		RESULT 12	
		: Sequence 1, Application US/10299327	
		: Publication No. US20030104482A1	
		: GENERAL INFORMATION:	
		: APPLICANT: Immunex Corp.	
		: APPLICANT: Bird, Timothy	
		: APPLICANT: Virca, G.D.	
		: TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS	
		: TITLE OF INVENTION: (DAKAR)	
		: FILE REFERENCE: 2889-US	
		: CURRENT APPLICATION NUMBER: US/10/299,327	
		: CURRENT FILING DATE: 2002-11-18	
		: PRIOR APPLICATION NUMBER: US/09/509,802	
		: PRIOR FILING DATE: 2000-06-02	
		: NUMBER OF SEQ ID NOS: 5	
		: SOFTWARE: PatentIn version 3.0	
		: SEQ ID NO 1	
		: LENGTH: 2370	
		: TYPE: DNA	
		: ORGANISM: Mus sp.	
		US-10-299-327-1	
		Alignment Scores:	
		Pred. No.: 8.09e-32 Length: 2370	
		Score: 410.50 Matches: 164	
		Percent Similarity: 43.43% Conservative: 84	
		Best Local Similarity: 28.72% Mismatches: 209	
		Query Match: 11.58% Indels: 116	
		DB: 9 Gaps: 25	
US-09-981-397A-16	(1-671) x US-10-299-327-1	(1-2370)	
QY	14 SerterSpheleuGluserrAlagluLeuAspSerGlygylPheglYlysValSerleu	33	
Dd	64 GCCCGCAAMTCCGAGCCTGGAGAAGTGCGCTCGGGCGCTTCGGGACGTGACAG	123	
	:		
QY	34 CysphenHisarGthrnglYleumetlleMetLysThr-----ValtyrLysoly	50	
Dd	124 GTGGGCCAT-----GTGCACGTGAGAACGTGCTGCGCATCAAGTCTCG	166	
	:		
QY	51 ProAnsGys---llegluHIsasngu-----AlaleuLeugluAlalysmetMet	67	
Dd	169 CCCAGTCTGCACGTGCAGCGACGAGCAAGCAAGTAGAGCTCTCGAGAGAGCTTAACAAGATG	228	
	:		
QY	68 AsnarGleuarGhtSerArGvalValLyLsleuleuGlyVallellegluglugLYlys	87	
Dd	229 GAGATGGCCAAGTCCGATACATTCACTGCTACCGCATGCCAGGAA-----CCT	282	
	:		
QY	88 TytserleuValmetGuiryrmetsLyrgIyasnleuMetHIsValleuLyalsAglu	107	
Dd	283 GTCCGCTTGCTCATGGATGATCATGGAGACAGGCTCCCTGGAGAAAGCTCTGAGCTCACAG	342	
	:		
QY	108 MetSerThrProleuSerValLySGlyArgilleleleuGluillelleglUGlymetCys	127	
Dd	343 ---CCATTGGCTTGGGAGCCTGCCCTTTCGCATCTGCACAGACAGACGCGTGGCATGAC	393	
	:		
QY	128 TytleuHIs-----GlyLySGlyVallleHIsLySAspleuLySProgluaSnlleu	145	
Dd	400 TTTCTGATGATGCATGTCTCCGCGACGTGCACCTAGACCTGAACCGCAACATCCTG	459	
	:		
QY	146 ValAsprsnAsphentHIsleuSllleHIsAsprleuGlyleuAlaserPhelysmetrPr	165	
Dd	460 CTGATATCCCACATPACATGTCACAGATTGTACTTTGGCTGGCTGGC-----	504	
	:		
QY	166 SerLySleuAsnsgluGluHIsasnguIlueArGrGluValAspGIThralALySlys	185	
Dd	505 ---AAGTGCATATGGCATGTCCCACTGTATGACCTCAGCATGAGATGGCGCTGT--	555	
	:		
QY	186 AsnclYglyThrleuTyrtYrMetalaprogluHIsleuAsnspValAsnalalySpro	205	


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Db 556 -----GGTACAAATCGCTTACCTCCCTCCAGAGCGCAATTCTGTGAGAGAGCGCTTGT
Oy 206 ThrGluysSerAspValTyrSerPheAlaValLeuTTPalaIllePheAlaSerLeu 225
Db 610 GACACCAACATGATGTATACAGCTTGGCCANTGTGAGTGGGTCTTACACAGAG 669
Oy 226 GluProTyrGluAsnAlaIlleCysGluGlnGlnLeuIleMetCysIlleLysSerGlyAsn 245
Db 670 AAGCCATTGGAGATGAAGAAGACATCTACACATCATGATGAAGTGGTAAAGGCCAC 729
Oy 246 ArgProAspValAspAspIleHcGluTyrCysProArg-----GluIleLysSer 262
Db 730 CGCCAGAGCTGCCACCATCTGCAGACCCCGCGCGCTGCTGTGCAGCGCTGATAGG 789
Oy 263 LeuMetLysLeuCysTyrPGLuAlaAsnProGluAlaArgProThrPheProGlyLleGlu 282
Db 790 CTCATGCAACGGTGTGTGCATGCAAGACCAACAGGTGGCCACCTTCCCAAGAAATTTACC 849
Oy 283 GluTyrPheArgProPheTyrLeuSerGlnLeuGlnGlnSerValGluGluAspValLys 302
Db 850 TCTGAA-----ACAGAGACCTTTGTGTGAGAACCCCTGATGAGAGAGTGA 894
Oy 303 SerLeuLysLysGluTyrSerAsnGluAsnAlaValLysArgMetGlnSerLeuGln 322
Db 895 GACCTGGCTCATGAGCCAGCGAGAAAGC-----TCTCTAGAG 933
Oy 323 LeuAspCysValAlaValPro---SerSerArgSerAsnSerAlaThrGluGlnProGly 341
Db 934 TCCAGAGAGTAGAGGCCCGAGCTCTCAGCGCTCAAGCGCGCTGCTCCCTCCCTTC 993
Oy 342 SerLeuHisSerSerGlnGlyLeuGlnMetGlyProValGlnGlnSerTyrPheAlaPro 361
Db 994 GATAACGACTGCAGCTCTCCGAGTGTCTGCACAGTTG---GACTCTGGGATCCAG 1050
Oy 362 SerLeuGlnHisProGlnGlnGluAsnGluProSerLeuGlnSerLeu---GlnAsp 380
Db 1051 ACTCTTGAGGCGCCGAGAGAGCTCAGCCGAGATTCCTGTGATGACAGCTCCCATCGTCC 1110
Oy 381 GluAlaAsnTyrHisLeuTyrGly---SerArgMetAspArgGlnThrLysGlnGlnPro 399
Db 1111 AGCAGTGGCAAGAGGCTCTCGGGGTCTCTCAGTGTGACTAGCCTTTCTCCAGAGGA 1170
Oy 400 ArgGlnAsnValAlaTyrAsnArgGlnGlnGluGluArgArgValSerHisAspPro 419
Db 1171 TCGCTGTACTGTCTTTGAGCGGGAAGCTTC-AACAGGCGA-----CCT 1214
Oy 420 PheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGlnGlyLysGlyThrValTyr 439
Db 1215 GGGCCCCACAGACATCCAGAGAA-----GAAGCTAGTGGATGCCATCAT 1259
Oy 440 SerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSer-----GlyLeu 455
Db 1260 -----ATCAGGGGAGACACCAGCGCTGATGAGATCTTACAGCCCCAAGATGTGGACTT 1313
Oy 456 ThrSer----- 457
Db 1314 GGTCTTAGACACAGCAGTGCACCTGCTCAGCTGTGAGAGCCGAGAGAGAGAGTGC 1373
Oy 458 -----GlnProGlnValLeuTyrGlnAsnAsnGlyLeu 468
Db 1374 TGTCAGTGGCTGTGTTAACAAATGCCAACCCCAACT---GACCACACAGAGAGAGGCTC 1430
Oy 469 Tyr---SerSerHisGlyPheGlyThr----- 476
Db 1431 TACACCACTGCATATGCTGTGTGAGCCGAGAGAGAGTGAATTTGAGACTACTGCTAGC 1490
Oy 477 -----ArgProLeuAsp---ProGlyThrAlaGlyP 486
Db 1491 CCGAGAGACAGTGTCAATGCCCAAGAGATGAAGACAGAGTGCCTTGGCACTTTGGCAGC 1550
Oy 486 TGAATGValTyrTyrArgProIleProSerHisMetProSerLeuHisAsnIleProValP 506

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Db 1551 CCAGATGGGGATGAGGCCAGCACAGGCTG-CTGCTAGAG---AAGATGCTTCTGTCA 1606
Oy 506 roGluThrAsnTyrLeuGlyAsnThrPro 515
Db 1607 ATGAGGTGACTTTTGAGGGCGGAGACACCC 1635

RESULT 13
US-10-152-661-257
; Sequence 257, Application US/10152661
; Publication No. US20030022835A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishnand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c5
; CURRENT APPLICATION NUMBER: US/10/152,661
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 09/866,050
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/221,232
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/206,650
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/312,283
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/NZ99/00051
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 09/188,930
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: 09/069,726
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 3516
; TYPE: DNA
; ORGANISM: Mouse
US-10-152-661-257

Alignment Scores:
Pred. No.: 1,456-31 Length: 3516
Score: 410.50 Matches: 164
Percent Similarity: 43.43% Conservative: 84
Best Local Similarity: 28.72% Mismatches: 209
Query Match: 11.58% Indels: 116
Gaps: 25

US-09-981-397A-16 (1-671) x US-10-152-661-257 (1-3516)
Oy 14 SerSerAspPheLeuGlnSerAlaGluAspSerGlyGlyPheGlyLysValSerLeu 33
Db 58 GCGGCGAATTCGCGAGGCTGGGAGAGGTGGGCTGGGCGGCTTGGCGAGGTGTACAG 117
Oy 34 CysPheHisArgThrGlnGlnGlyLeuMetIleMetLysThr-----ValTyrLysGly 50
Db 118 GTGGCGCAT-----GTGCACGTGGAAGCTGGCTGCGCATCAAGTGCCTG 162
Oy 51 ProAsnCys---LleGlnHisAsnGlu-----AlaLeuGlnGluAlaLysMetMet 67
Db 163 CCCAGTCTGCAGCTGCGAGACAGGAGCAATGAGTCTGTGAGAGAGCTAAGAGATG 222
Oy 68 AsnArgLeuArgHisSerArgValValLysLeuLeuGlyValIleLleGlnGlnGlyLys 87
Db 223 GAGATGCCCAAGTCCGATACATTTCTACTGTGTACGCAATATGCCAGAA-----CCT 276
Oy 88 TyrSerLeuValIleMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLysAlaGlu 107
Db 277 GTGGGCTTGTGCATGAGTACATGAGACAGGCTCCCTGTGAGAGAGCTGCTGGCTCAGAG 336

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OY 108 MetSerThrProLeuSerValIysGlyArgIleIleLeuGluIleIleGluIleMetCys 127
Db 337 ---CCATGGCTTGGGACCTGGCGTTGGCATCTGGACAGACAGACCCCTGGGCATGAC 393
OY 128 TyrLeuHis-----GlyLysGlyValIleHisLysAspLeuLysProGluAsnIleLeu 145
Db 394 TTCGTCGATTCGATCTCTCCGCCACTGCTGACCTAGACCTGAAAGCAGCAACATCTCTG 453
OY 146 ValAspAsnAppPheHisIleLeuLysIleAlaAspLeuGlyLeuAlaSerPheLysMetTrp 165
Db 454 CTGGATGCCACCTACCATCTCAGATTTCTGACTTTGGCTGGCC----- 498
OY 166 SerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAlaSpGlyThrAlaLys 185
Db 499 ---AAGTCGAATGGCATGTCCTCATGACCTCAGCATGATGGCTGTT----- 549
OY 186 AsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLysAsnAspValAlaAsnIlePro 205
Db 550 -----GGTACATGCTTACCTCCCTCCAGAGCAATCTGAGAGAGCCGCTTGT 603
OY 206 ThrGluLysSerAspValTyrSerPheAlaValIleLeuTrpAlaIlePheAlaAsnLys 225
Db 604 GACACCAACATGATGATATACAGCTTCGCACTTGATCTGGGCTGCTTACACAGAG 663
OY 226 GluProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCysIleLysSerGlyAsn 245
Db 664 AAGCATTTGCAGATGAAGAAAGAACATCTACACATCATGATGAAGTGAAGGCCAC 723
OY 246 ArgProAspValAlaAspIleThrIuTyrCysProArg-----GluIleLeuSer 262
Db 724 CGCCGAGCGCCACCCATCTGACAGCCCGCGCTGCTGCTGACAGCTGATGAGG 783
OY 263 LeuMetLysLeuCysTyrGluAlaAsnProGluAlaIleValIleProThrPheProGlyIleGlu 282
Db 784 CTCATGCAACGCTGCTGGCATGACACCCACAGCGCGCCACCTCCACAGAAATTCAC 843
OY 283 GluLysPheArgProPheTyrLeuSerGluLeuGluGluIleValIleGluAspValLys 302
Db 844 TCTGAA-----ACAGAGACCTTTGTGAGAGAGCCGATGAGAGAGGTGA 888
OY 303 SerLeuLysGluTyrSerAsnGluAsnAlaValIleLysArgMetGluSerLeuGlu 322
Db 889 GACCTGGCTCATGACCCAGCGGAGCAAAAG-----TCTCTAGAG 927
OY 323 LeuAspCysValAlaValPro---SerSerArgSerAsnSerAlaThrGluGluProGly 341
Db 928 TCCAAGATGAGGCCAGGCCGAGCTCTCAGCCCTCAAGCGGCTCTGCTCCCTTC 987
OY 342 SerLeuHisSerSerGluGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaPro 361
Db 988 GATAACGACTGACGCTCTCCGAGTTGCTGCACAGTTG---GACTCTGGGAGTCCAG 1044
OY 362 SerLeuGluHisProGluGluGluAsnGluProSerLeuGluSerLysLeu---GluAsp 380
Db 1045 ACTCTTGAAGCCCGGAGAGCTCAGCCGAAATTCCTCTGATGACCACTCCATCTGCC 1104
OY 381 GluAlaAsnTyrHisLeuTyrGly---SerArgMetAspArgGluThrLysGluGluPro 399
Db 1105 AGCAGTGGCAAGAGGCTCTGGGGGTGCTCAGTGGCTCAGAGCTTCTTCCACAGAGA 1164
OY 400 ArgGluAsnValAlaTyrAsnArgGluGluGluArgArgArgValSerHisAspPro 419
Db 1165 TCGCTGCTACTGCTTTTGGAGCGGAACTTC-AAACAGGCA-----CCT 1208
OY 420 PheAlaGluGluArgProTyrGluAsnPheGluAsnThrGluGlyLysGlyThrValTyr 439
Db 1209 GGGCCCAACAGACATCCAGAGAA-----GAAGCAGTGGATGCCATCAT 1253
OY 440 SerSerAlaIleSerHisGlyAsnAlaValHisGluProSer-----GlyLeu 455
Db 1254 -----ATCAGGGGACACACAGGCTGATGAGATCTTACAGCCCAAGATGTGGACTT 1307

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OY 456 ThrSer----- 457
Db 1308 GGTTCATGACACAGATGCGACCTGCTGCACTGGCTGGAGCGGAGACAGACTG 1367
OY 458 -----GluProGluValLeuTyrGluAsnAsnGlyLeu 468
Db 1368 TGTCAAGTGGCTGCTGCTTAACATGACCAACCCCAACCT---GACCAACAGAGAGGCTC 1424
OY 469 Tyr---SerSerHisGlyPheGlyThr----- 476
Db 1425 TACACCATGCTGATGCTGTGTGAGCGGAGGAGCTGGAATTTGGAGCTACTGCTAGC 1484
OY 477 -----ArgProLeuAsp--ProGlyThrAlaGlyP 486
Db 1485 CCGAAGACCACTGTCATGCCAAGATGAAACACAGTGGAGTGGCTGCACTTGGCAGC 1544
OY 486 roArgValIleTyrArgProIleProSerHisMetProSerLeuHisAsnIleProValP 506
Db 1545 CCAGATGGGAGATGAGGCCAGCACAGGCTG-CTGCTAGAG---AAGATGCTTCTGTCA 1600
OY 506 roGluThrAsnTyrLeuGluAsnThrPro 515
Db 1601 ATGAGTGGACTTGTGAGGCGGAGACACC 1629

RESULT 14
US-09-866-050A-257
; Sequence 257, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions isolated from skin cells
; FILE REFERENCE: 11000.1011c4U
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 3516
; TYPE: DNA
; ORGANISM: Mouse
US-09-866-050A-257

Alignment Scores:
Pred. No.: 1,45e-31 Length: 3516
Score: 410.50 Matches: 164
Percent Similarity: 43.43% Conservative: 84
Best Local Similarity: 28.72% Mismatches: 209
Query Match: 11.58% Indels: 116
DB: 9 Gaps: 25

US-09-981-397a-16 (1-671) x US-09-866-050A-257 (1-3516)
OY 14 SerSerAspPheLeuGluSerAlaGluLeuAspSerGlyGlyPheGlyLysValSerLeu 33
Db 58 GCGGCGCAATTCGAGAGCTGCGAGAGAGTGGCTGGCGGCTTGGGACAGCTTACAG 117
OY 34 CysPheHisArgThrGluGluGlyLeuMetIleMetLysThr-----ValTyrLysGly 50
Db 118 GTGGCCCAT-----CTGCACTGGAAGAGTGGCTGGCATCACTGCTGCTG 162
OY 51 ProAsnCys---IleGluHisAsnGlu-----AlaLeuGluGluGluAlaLysMetMet 67
Db 163 CCCAGTCTGCACGCTGCGAGACAGGAGAACGAATGAGACTCTCTGGAGGAGTAAAGAGATG 222
OY 68 AsnArgLeuArgHisSerArgValValLysLeuGluGlyValIleIleGluGluGlyLys 87
Db 223 GAGATGGCGCAAGTTCGATACATATTCACCTGTGTACGGCAATATCCAGGAA-----CCT 276

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QY 88 TyrSerLeuValMetGluTyrMetGluValAsnLeuMetHisValLeuLysAlaGlu 107
    |||||
Db 277 GTGGCGTGGTGCATGAGTACATGAGACAGAGCGCTCCCTGGAGAAAGCTGCTGCTCAGAG 336
    |||||
QY 108 MetSerThrProLeuSerValLysGlyArgIleIleLeuGluIleIleGluLysMetCys 127
    |||||
Db 337 ---CATTGGCTTGGAGCTGCTCCCTTGGCATGCTGACAGACAGACCGTGGCATGAC 393
    |||||
QY 128 TyrLeuHis-----GlyLysGlyValIleHisLysProLeuLysProGluAsnIleLeu 145
    |||||
Db 394 TTCCCTGATTGCATGCTCCGCCACCTGCTCACCCTAACCTGAAGCCAGGCAACATCCTG 453
    |||||
QY 146 ValAspAsnAspPheHisIleLysIleAlaAspLeuGluLeuAlaSerPheLysMetTrp 165
    |||||
Db 454 CTGATGCCACACATGACATGTCAGATTTGACTTGGCTGGCC----- 498
    |||||
QY 166 SerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAspGlyThrAlaLysLys 185
    |||||
Db 499 ---AAGTGCATGATGCATGCTCCACTCTCATGACCTGCATGATGAGCTGCTTT----- 549
    |||||
QY 186 AsnGlyLysThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAsnAlaLysPro 205
    |||||
Db 550 -----GGTACAAATCGCTTACCTCCCTCCAGAGGAATTCGTGAGAAAGCCGCTTGT 603
    |||||
QY 206 ThrGluLysSerAspValTyrSerPheAlaValValLeuTrpAlaIlePheAlaAsnLys 225
    |||||
Db 604 GACACCAAAACATGATGATACAGCTTGCATTTGTGCTGGGTGCTTACACAGAG 663
    |||||
QY 226 GluProTyrGluAsnAlaIleCysGluGluGluLeuIleMetCysIleLysSerGlyAsn 245
    |||||
Db 664 AAACCATTTGCATGAAAGAACATCTACACATCATGATGAAAGTGAAGAGGCGCAC 723
    |||||
QY 246 ArgProAspAlaAspAlaIleThrGlyCysProArg-----GluIleIleSer 262
    |||||
Db 724 CGCCACAGCTGCCACCATCTGCAGACCCCGCGGCTGCTGCCAGCGTATAGCG 783
    |||||
QY 263 LeuMetLysLeuCysTrpGluAlaAsnProGluAlaArgProThrPheProGlyIleGlu 282
    |||||
Db 784 CTCATGCAAGCGTGTGATGACGACACAGCTGGCGCCACCTTCCAAAGAAATTAC 843
    |||||
QY 283 GluLysPheArgProPheTyrLeuSerGluLeuGluLysSerValGluLysAspValLys 302
    |||||
Db 844 TCTGAA-----ACAGAAGACCTTTGTGAGAAGCCTGAGAGAGAGCTGAAA 888
    |||||
QY 303 SerLeuLysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGlnSerLeuGln 322
    |||||
Db 889 GACCTGGCTCATGAGCGCAGGAGAAAGC-----TCTCTAGAG 927
    |||||
QY 323 LeuAspCysValAlaValPro-----SerArgSerAsnSerAlaThrGluGlnProGly 341
    |||||
Db 928 TCCAGAGTGAAGCGCCAGCGGAGTCTCTCAGCGCTCAAGCGCGCTGCTGCCCTTC 987
    |||||
QY 342 SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluLysSerTrpPheAlaPro 361
    |||||
Db 988 GATAACAGACTGACGTCTCTCCGAGTTCTGTCAACAGTTG---GACTCTGGAGATCTCCAG 1044
    |||||
QY 362 SerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeu---GlnAsp 380
    |||||
Db 1045 ACTCTTGAAGCGCCCGAGAGCTCAGCGGAGATTCTCTAATGCAAGCTCCCATCTGCC 1104
    |||||
QY 381 GluAlaAsnTyrHisLeuTyrGly---SerArgMetAspArgIleThrLysGlnPro 399
    |||||
Db 1105 AGCAGTGGCAAGAGGCTCTGGGGGTCTCTCAGTGAACATCAGCTTCTCCAGAGAGA 1164
    |||||
QY 400 ArgGluAsnValAlaTyrAsnArgGluGluGluArgArgArgValSerHisAspPro 419
    |||||
Db 1165 TCCCTGTCACTCTTTTGGAGCGGAGCTTC---AACAGCGCA-----CCT 1208
    |||||
QY 420 PheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyr 439
    |||||
Db 1209 GGGCCCCACAGACATCCAGAGAA-----GAAAGTACTGATGCCATCAT 1253
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QY 440 SerSerAlaAlaSerHisGlyAsnAlaValHisInProSer-----GlyLeu 455
    |||||
Db 1254 -----ATCAGGGGACACACACAGAGCTGATGATGATCTTACAGCCCAAGATGTGACTT 1307
    |||||
QY 456 ThrSer----- 457
    |||||
Db 1308 GGTCTGTAGACAGCAGTGCCACCTGTGTGACACTGGTGTGGAGCCGAGACGAGAGATG 1367
    |||||
QY 458 -----GlnProGlnValLeuTyrGlnAsnAsnGlyLeu 468
    |||||
Db 1368 TGTCAAGTGGCTGTCTTAACTGCAATGCCAACCCCACT---GACCAACAGAGAGGCTC 1424
    |||||
QY 469 Tyr---SerSerHisGlyPheGlyThr----- 476
    |||||
Db 1425 TACACACATGATGTGCTGTGGAGCGGAGAGGAGCTGATTTGAGACTACTGTAC 1484
    |||||
QY 477 -----ArgProLeuAsp---ProGlyThrAlaGly 486
    |||||
Db 1485 CCGGAGACAGCTGCAATGCCAGAGATGAGAGACAGTGAAGAGCTGCTGCTTGCAGC 1544
    |||||
QY 486 roArgValTTPtyrArgProIleProSerHisMetProSerLeuHisAsnIleProValP 506
    |||||
Db 1545 CCAGAAATGGGAGTGGAGCCACAGACAGGCTG---CTGCTAGAG---AAGAAATGCTTCTGTCA 1600
    |||||
QY 506 roGluThrAsnTyrLeuGlyAsnThrPro 515
    |||||
Db 1601 ATGAGTGGACTTTGAGGCGGAGACACCC 1629
    |||||

RESULT 15
US-10-152-661-510
: Sequence 510, Application US/10152661
: Publication No. US2003022835A1
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorina
: APPLICANT: Sleeman, Matthew
: APPLICANT: Ormest, Rene
: APPLICANT: Murison, James G.
: APPLICANT: Kumble, Krishanand D.
: TITLE OF INVENTION: Compositions and Methods for Isolating From Skin Cells
: FILE REFERENCE: 11000.10115
: CURRENT APPLICATION NUMBER: US/10/152,661
: PRIOR FILING DATE: 2002-05-20
: PRIOR APPLICATION NUMBER: 09/866,050
: PRIOR FILING DATE: 2001-05-24
: PRIOR APPLICATION NUMBER: 60/221,232
: PRIOR FILING DATE: 2000-07-25
: PRIOR APPLICATION NUMBER: 60/206,650
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: 09/312,283
: PRIOR FILING DATE: 1999-05-14
: PRIOR APPLICATION NUMBER: PCT/NZ99/00051
: PRIOR FILING DATE: 1999-04-29
: PRIOR APPLICATION NUMBER: 09/188,930
: PRIOR FILING DATE: 1998-11-09
: PRIOR APPLICATION NUMBER: 09/069,726
: PRIOR FILING DATE: 1998-04-29
: NUMBER OF SEQ ID NOS: 725
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 510
: LENGTH: 1700
: TYPE: DNA
: ORGANISM: Rat
US-10-152-661-510

Alignment Scores:
Pred. No.: 6 27e-32 Length: 1700
Score: 409.50 Matches: 156
Percent Similarity: 38.77% Conservative: 84
Best Local Similarity: 25.20% Mismatches: 178
Query Match: 11.55% Indels: 201
DB: 9 Caps: 29

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US-09-981-397A-16 (1-671) x US-10-152-661-510 (1-1700)

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OY 5 MetSerLeuAsnValIleLysMet-----LysSerSerAspPheLeuGlu 19
Db CTCTGGATGCTTCTTCAGATATAGCTCAATGCTGCTCATCTCTCTGCGC 183
OY 20 SerIleGluLeuAspSer-----GlyGlyPheGlyLysValSerLeu 33
Db TCTGAGAGACTGGAGAACCTTAGAGATTGTGGCAAGCGGGGTGGAGCCGTGTCGG 243
OY 34 CysPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGlyProAsnGly 53
Db GCACGCCACACAGCATGAGACCTTGATGAGCATGAGCAAG----- 282
OY 54 IleGlnHisAsnGluAlaLeuLeuGluGluAlaLysMetMetAsnArgLeuArgHisSer 73
Db ATCGTAACCTCGAAGAGATATCCAGGAGGTGAAGGCTATGCTGAATCTTGTCATGAG 342
OY 74 ArgValValLysLeuLeuGlyValIleIleGlu---GlnGlyLysTyr----- 88
Db AACGTCGCTCTCTCTGCGGCTCAGTGAACCTCGAGTGGAGTACGTGACGGCGC 402
OY 89 SerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeuLysAlaGluMet 108
Db GCTCTGTGACAGATGATGAGAGAACGCTCTCTGAGGCTCTGCAACCTTCATGTC 462
OY 109 SerThrProLeuSerValLysGlyArgIleIleLeuGluIleIleGlnGlyMetCysTyr 128
Db CCTCGGCGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
OY 129 LeuHis-----GlyLysGlyValIleHisLysAspLeuLysProGluAsnIleLeuVal 146
Db CTACACAGCTTGACCCCTTGCTACTGACCGGAGCCTCAAGCCCTCAATGTTCTGCG 582
OY 147 AsparAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLysMetTrpSer 166
Db GATTCAGAGCTCCAGCCAGATGAGCATTTGGCTGCTGCTGCTGCTGCTGCTGCTG 642
OY 167 LysLeuAsnAsnGluGlnHisAsnGluLeuArgGluValAspGlyThrAlaLysLysAsn 186
Db CAGTCAGGCTCA-----GGGTCAGATCGAGACATCT 675
OY 187 GlyIleThrLeuTyrTyrMetAlaProGluHisLeuAsnAspValAsnAlaLysProThr 206
Db GGGGACCCCTGACTTACTTGGCCACAG---CTGTCGATTAATGACGGAAGGCTCT 732
OY 207 GlnLysSerAspValTyrSerPheAlaValLeuThrPalaIlePheHisAsnLysGlu 226
Db AAAGCAAGTATGTTTACAGTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 792
OY 227 Pro-----TyrGluAsnAlaIleCysGlnGlnGlnLeuIle 238
Db GGTGAGGTGTAGACAGACCTCACAATTCGTGAGGAGCTGTGAACAGGAG----- 846
OY 239 MetCysIleLysSerGlyAsnArgProAspValAspPheIleThrGluTyrCysProArg 258
Db AGCGACCTCCATTCATGACAGACCTCCCGGACAGACCCCTGAG 888
OY 259 Glu-----IleIleSerLeuMetLysLeuCysTrpGluAlaAsnProGlu 273
Db ACTCTGGCTTGAAAGGACTGAAGAGATTAAATGACGCAATGCTGAGGATTCTGAGCCTTAA 948
OY 274 AlaArgProThrPheProGlyIleGlnGluLysPheArgProPheTyrLeuSerGlnLeu 293
Db GACAGGCACTCTCCAAAGACGTGAATCAAAAACCAATATGTTTACATC---CTGCTA 1005
OY 294 GlnGluSerValGlnGluAspValLysSerLeuLys-----LysGluTyrSerAsn 310
Db CAGGACAAAGTAGTGTCTGCTCCAGGTAAGCATTAATCTGCTCAGTACAGAAC 1065
OY 311 GluAsnAlaValValLysArgMetGlnSerLeuGln-----LeuAspCysVal 326

```

```

Db 1066 AGTACACAAGATTGTCTGCCAGAGAGTCCAGCCAAAAGAGTACAGAGTGCATTGC--- 1122
OY 327 AlaValProSerSerArgMetAspArgSerAlaThrGlnGlnProGlySerLeuHisSerSer 346
Db -----CCGAGGGAAACCACTACTTTATGAATGCTGAGCCGCTGCAT----- 1164
OY 347 GlnGlyLeuGlyMetGlyProValGlnGluSerThrPheAlaProSerLeuGluHisPro 366
Db 1165 -----CTGAGAGAGGCC 1176
OY 367 GlnGlnGluAsnGlnProSerSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeu 386
Db 1177 TCT----- 1179
OY 387 TyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsn 406
Db 1180 ---GGATCAGTCTCTGAAAGACTCAAGACTT----- 1209
OY 407 ArgGlnGlnGluArgArgArgValSerHisAspProPheAlaGlnGlnArgProTyr 426
Db 1209 ----- 1209
OY 427 GluAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSerSerAlaAlaSerHisGly 446
Db 1210 -----ACTGAGAGAGAGCA-----AGGAGCATCATTTGG 1242
OY 447 AsnAlaValHisGlnProSerGlyLeuThrSerGln-----ProGlnVal 461
Db CATGCGACA-----CCAGCAGGAGCATCTGACCTGCGTGGCAGCTCCCAAT 1296
OY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
Db 1297 CCACAT-----ACTTACCCTCCAGAGCCACAGACCAACCTAGGCGACCTTTACT 1344
OY 482 GlyThrAlaGlyProArgValTyrPyrArgProIleProSerHisMetProSerLeuHis 501
Db 1345 GAGACTCCAGGCTCTGAC----- 1362
OY 502 AsnIleProValProGluThrAsn-----TyrLeu 511
Db 1363 -----CCCCAAAGGATCAGGAGATGAGAACAGCAACGCAATCTGTCACACC 1410
OY 512 GlyAsnThrProThrMetProPheSerSerLeuProProThrAspGluSerIleLysTyr 531
Db 1411 TGGAAAGCAGCCAAAT---CCAATGACAGGCTA-----CAGCTCATTT----- 1449
OY 532 ThrIleTyrAsnSerThrGlyIleGlnIleGlyAlaTyrAsnTyrMetGluIleGlyGly 551
Db 1450 GTCTTAACACACTGTTCTGAAAGTGCAGATTGCACAACACACTGCATGTCACTA----- 1503
OY 552 ThrSerSerSerLeuLeuAspSerThrAsnThrAsnPro---LysGlnGluProAla 569
Db 1504 -----CAACCGAAGAACTGCTTCCCAAGAGAGGAGCAGCA 1539

```

Search completed: June 25, 2003, 23:47:51
 Job time : 275 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2003, 16:07:14 ; Search time 43 Seconds
(without alignments)
1500.144 Million cell updates/sec

Title: US-09-981-397A-16

Perfect score: 3545
Sequence: 1 MOPDMSLVNVIKMKSSDFLES.....ALHOCSDRLDLSLIVYSON 671

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	3545	100.0	671	2 T09479	serine/threonine p
2	2423.5	68.4	656	2 T49299	receptor interacti
3	346.5	9.8	1367	1 IGHUR1	insulin-like growt
4	343	9.7	467	2 T56579	protein-tyrosine k
5	342.5	9.6	640	2 S23008	insulin-like growt
6	340.5	9.6	855	2 T20082	hypothetical prote
7	338.5	9.5	465	2 T48926	protein-tyrosine k
8	338.5	9.5	505	2 T59296	protein-tyrosine k
9	338	9.5	1371	2 A33837	insulin-like growt
10	337.5	9.5	507	2 A55625	protein-tyrosine k
11	336.5	9.5	848	2 B87950	protein F33E2.2 [i
12	336.5	9.5	1171	2 T12956	hypothetical prote
13	335	9.4	512	1 TYHUIY	protein-tyrosine k
14	335	9.4	829	2 T07406	probable protein k
15	334.5	9.4	1094	2 S49313	protein kinase - s
16	333	9.4	1382	1 INHUR	insulin receptor p
17	332.5	9.4	1372	2 A34157	insulin receptor p
18	331.5	9.4	390	2 T01451	protein kinase hom
19	330.5	9.3	1383	2 A36080	insulin receptor p
20	330.5	9.3	2148	1 A56081	insulin receptor p
21	329.5	9.3	475	2 T12955	probable protein k
22	329	9.3	1257	2 T00486	serine/threonine-s
23	328.5	9.3	450	1 S15094	protein-tyrosine k
24	328.5	9.3	567	1 JCS957	transforming growt
25	327.5	9.2	1248	2 B96827	hypothetical prote
26	327.5	9.2	2101	2 S57245	insulin receptor k
27	325.5	9.2	507	1 A39339	protein-tyrosine k
28	325	9.2	512	1 A39719	transforming growt
29	325	9.2	606	2 JC5956	transforming growt

30	324.5	9.2	497	1 S43532	protein-tyrosine k
31	323.5	9.1	450	1 JH0559	protein-tyrosine k
32	322	9.1	512	1 I56160	protein-tyrosine k
33	322	9.1	1123	2 A39962	kinase-related tra
34	322	9.1	1125	1 OXURCP	spectact receptor p
35	321.5	9.1	509	1 OKHUKL	protein-tyrosine k
36	321.5	9.1	1147	2 F86297	hypothetical prote
37	320.5	9.0	579	2 JC5955	transforming growt
38	319	9.0	650	1 JC1450	fibroblast growth
39	318	9.0	450	2 A41973	protein-tyrosine k
40	318	9.0	942	2 C96574	hypothetical prote
41	317.5	9.0	407	2 G84635	probable protein k
42	317.5	9.0	450	2 T48929	protein-tyrosine k
43	317	8.9	1029	2 H86179	hypothetical prote
44	316.5	8.9	625	1 A43030	protein-tyrosine k
45	316	8.9	829	2 JC4583	fibroblast growth

ALIGNMENTS

RESULT 1
T09479
serine/threonine protein kinase (EC 2.7.1.-) RIP - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C:Accession: T09479; I38992
R:Huag, J.; Hsu, H.; Balchwal, V.R.; Goeddel, D.V.
submitted to the EMBL Data Library, August 1998
A:Reference number: 216685
A:Accession: T09479
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-671 <HUA>
A:Cross-References: EMBL:U50062; NID:93426026; PID:93426027
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
Cell 81, 513-523, 1995
A:Title: RIP: a novel protein containing a death domain that interacts with Fas/Apo-1
A:Reference number: A56913; MUID:95277838; PMID:7538908
A:Accession: I38992
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 300-513, 'S', 515-671 <RES>
A:Cross-References: EMBL:U25994; NID:9829616; PID:AA050137.1; PID:9829617
C:Genetics:
A:Gene: RIP
C:Keywords: ATP binding; phosphotransferase
Query Match 100.0%; Score 3545; DB 2; length 671;
Best Local Similarity 100.0%; Pred. No. 1.7e-161;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOPDMSLVNVIKMKSSDFLESALDSGGFGKYSLCFHRTOGLIMTKYKGPNCIEHNEAL 60
DB 1 MOPDMSLVNVIKMKSSDFLESALDSGGFGKYSLCFHRTOGLIMTKYKGPNCIEHNEAL 60
QY 61 LEEAKMNRRLRSRYKVLGVLIEGKYSLVWEYHEKGNLHVLAENSTPLSVAGRIIL 120
DB 61 LEEAKMNRRLRSRYKVLGVLIEGKYSLVWEYHEKGNLHVLAENSTPLSVAGRIIL 120
QY 121 EIIIEGMCYIAGKGVVHKDLKPEIIVLNDNFHRIKIDGLASFKMMSKLNNEHNLREVD 180
DB 121 EIIIEGMCYIAGKGVVHKDLKPEIIVLNDNFHRIKIDGLASFKMMSKLNNEHNLREVD 180
QY 181 GTAKRNGGLTYMADEHLNDVNAKPTKESDVYSFAVVLMAIFANKEPYENALICEQOLIMC 240
DB 181 GTAKRNGGLTYMADEHLNDVNAKPTKESDVYSFAVVLMAIFANKEPYENALICEQOLIMC 240
QY 241 IKSGNRPPVDOTTECPREIISLMKLCWEANEAPRTPTGTEKRRPYLSOLESVED 300
DB 241 IKSGNRPPVDOTTECPREIISLMKLCWEANEAPRTPTGTEKRRPYLSOLESVED 300
QY 301 VKSLKKEYSNEAVVAKRMQSLQLDCAVAVSSRSNSATBQPSGLHSSQGLGMGPVEESWFA 360

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Db      301 VKSLKREYSENAVYKRMQSLQDCVAVPSSRSNSATEQPGSLHSSQGLMGPEESWFA 360
QY      361 PSLERHOENEPESLSQSLQDEANHYLYGSRMDROT KOOPRONVAVNREERRRRVSHDF 420
Db      361 PSLERHOENEPESLSQSLQDEANHYLYGSRMDROT KOOPRONVAVNREERRRRVSHDF 420
QY      421 MOORPYENFONTEGKGYVSSAASHGNVAHQPSGLTSOPQVLYONNGLYSSHGFGTRPLD 480
Db      421 MOORPYENFONTEGKGYVSSAASHGNVAHQPSGLTSOPQVLYONNGLYSSHGFGTRPLD 480
QY      481 PGTAAPRWYRPIPSHMSPLHNPVETNYLGNTPTMPFSSLPPTDESIKTYTINSTGIC 540
Db      481 PGTAAPRWYRPIPSHMSPLHNPVETNYLGNTPTMPFSSLPPTDESIKTYTINSTGIC 540
QY      541 IGAVYMEIGTSSSLDSTNTNFKPEPAKYOALFDNTTSLTDKHLDPRENLGKHMKN 600
Db      541 IGAVYMEIGTSSSLDSTNTNFKPEPAKYOALFDNTTSLTDKHLDPRENLGKHMKN 600
QY      601 CARLIGFTQSOIDEIDHDYERDGLKEKYQMLQKVMREGLKATVGLAQLAHQCSRID 660
Db      601 CARLIGFTQSOIDEIDHDYERDGLKEKYQMLQKVMREGLKATVGLAQLAHQCSRID 660
QY      661 LLSLIYVSQN 671
Db      661 LLSLIYVSQN 671

```

RESULT 2

149299

receptor interacting protein RIP - mouse

C:Species: Mus musculus (house mouse)

C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999

C:Accession: I49299

R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.

Cell 81, 513-523, 1995

A:Title: RIP: a novel protein containing a death domain that interacts with Fas/ABO-1 (C

A:Reference number: A56913; MUID:95278783; PMID:7538908

A:Accession: I49299

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-656 <RES>

A:Cross-references: EMBL:U25995; NID:9829618; PIDN:AAB60487.1; PID:9829619

C:Genetics:

A:Gene: RIP

A:Superfamily: protein kinase homology

F:15-293/Domain: protein kinase homology <KIN>

Query Match 68.4%; Score 2423.5; DB 2; Length 656;

Best Local Similarity 69.8%; Pred. No. 3.4e-108;

Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

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QY      1 MOPDMSLVIVKMKSSDFLEASLDGSGFGKVSICPHRTGIMTKYKGCNCLIEHNAL 60
Db      1 MOPDMSLVIVKMKSSDFLEASLDGSGFGKVSICPHRTGIMTKYKGCNCLIEHNAL 60
QY      61 LEEAKMNRRLHRSRVKLLGVYIEEGKSYLMEYMEKGNLHVLAKESTPLSVGRITL 120
Db      61 LEEAKMNRRLHRSRVKLLGVYIEEGKSYLMEYMEKGNLHVLAKESTPLSVGRITL 120
QY      121 EELGCMCLHDKGVYHKDLKPEMLIVDFHIKTIADLVASFKTWSKLTKEKDKMKQKYS 180
Db      121 EELGCMCLHDKGVYHKDLKPEMLIVDFHIKTIADLVASFKTWSKLTKEKDKMKQKYS 180
QY      181 GTAKK-NGSTLYAPAEHLNDVNAKPTREKSDVYSAAVVLMTAFANKKEYEMALCEQOLIM 239
Db      181 GTAKK-NGSTLYAPAEHLNDVNAKPTREKSDVYSAAVVLMTAFANKKEYEMALCEQOLIM 239
QY      240 CIKSGNRDVDITETECREILISLKLCEANPEARPTPEIEKFRFYLSOLEESVEE 299
Db      240 CIKSGNRDVDITETECREILISLKLCEANPEARPTPEIEKFRFYLSOLEESVEE 299
QY      300 DYKSLKREYSENAVYKRMQSLQDCVAVPSSRSNSATEQPGSLHSSQGLMGPEESW 359
Db      300 DYKSLKREYSENAVYKRMQSLQDCVAVPSSRSNSATEQPGSLHSSQGLMGPEESW 359

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Db      301 DVASLKREYSDQSPVLQHRMFLSQHDCVPLPERSNS--EQGSLHSSQGLMGPEESWF 358
QY      360 APSLHROENEPESLSQSLQDEANHYLYGSRMDROT KOOPRONVAVNREERRRRVSHDP 419
Db      360 APSLHROENEPESLSQSLQDEANHYLYGSRMDROT KOOPRONVAVNREERRRRVSHDP 419
QY      420 FAOQAPRYENFONTEGKGYVSSAASHGNVAHQPSGLTSOPQVLYONNGLYSSHGFGTRPL 479
Db      420 FAOQAPRYENFONTEGKGYVSSAASHGNVAHQPSGLTSOPQVLYONNGLYSSHGFGTRPL 479
QY      480 PGTAAPRWYRPIPSHMSPLHNPVETNYLGNTPTMPFSSLPPTDESIKTYTINSTGIC 539
Db      480 PGTAAPRWYRPIPSHMSPLHNPVETNYLGNTPTMPFSSLPPTDESIKTYTINSTGIC 539
QY      540 OIGAVYMEIGTSSSLDSTNTNFKPEPAKYOALFDNTTSLTDKHLDPRENLGKHMKN 599
Db      540 OIGAVYMEIGTSSSLDSTNTNFKPEPAKYOALFDNTTSLTDKHLDPRENLGKHMKN 599
QY      600 NCARLIGFTQSOIDEIDHDYERDGLKEKYQMLQKVMREGLKATVGLAQLAHQCSRI 659
Db      600 NCARLIGFTQSOIDEIDHDYERDGLKEKYQMLQKVMREGLKATVGLAQLAHQCSRI 659
QY      660 DLSLIYVSQN 671
Db      660 DLSLIYVSQN 671

```

RESULT 3

149299

Insulin-like growth factor 1 receptor precursor - human

N:Alternate names: IGF-1 receptor

N:Contains: insulin-like growth factor 1 receptor alpha chain; insulin-like growth fa

C:Species: Homo sapiens (man)

C:Date: 24-Jun-1987 #sequence_revision 10-May-1996 #text_change 18-Feb-2000

C:Accession: A25690; B38268; PQ0159; A54170; B54170

R:Ullrich, A.; Gray, A.; Tam, A.W.; Yang-Feng, T.; Tsubokawa, M.; Collins, C.; Henzel

EMBO J. 5, 2503-2512, 1986

A:Reference number: A25690; MUID:87053815; PMID:2877871

A:Accession: A25690

A:Molecule type: mRNA

A:Residues: 1-1367 <ULL>

A:Cross-references: EMBL:M24599; GB:X04434; NID:933058; PIDN:CAA28030.1; PID:9804990

A:Experimental source: Placenta

A:Note: parts of this sequence were confirmed by peptide sequencing

R:Partanen, J.; Mekelae, T.P.; Alltalo, R.; Lehtvaesalho, H.; Alltalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A:Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.

A:Reference number: A38268; MUID:91062389; PMID:2247464

A:Accession: B38268

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1137-1193 <PAR>

R:Cooke, D.W.; Bankert, L.A.; Roberts Jr., C.T.; LeRoith, D.; Casella, S.J.

Biochem. Biophys. Res. Commun. 177, 1113-1120, 1991

A:Title: Analysis of the human type I insulin-like growth factor receptor promoter re

A:Reference number: PQ0159; MUID:91282751; PMID:1711844

A:Accession: PQ0159

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-31 <COO>

A:Cross-references: GB:M69229; NID:9184837; PIDN:AAB5399.1; PID:9184838

R:Kasuya, J.; Paz, I.B.; Maddux, B.A.; Goldfine, I.D.; Hetta, S.A.; Fujita-Yamaguchi,

Biochemistry 32, 13531-13536, 1993

A:Title: Characterization of human placental insulin-like growth factor-I/insulin h**yb**

A:Reference number: A54170; MUID:94079885; PMID:8257688

A:Accession: A54170

A:Molecule type: protein

A:Experimental source: Placenta

A:Note: sequence extracted from NCBI backbone (NCBIP:141172) and corrected to corres

A:Accession: B54170

A:Molecule type: protein

A:Residues: 741746,'X',748-750 <KA2>
A:Experimental source: placenta
C:Genetics:
A:Gene: GDB:IGF1R
A:Cross-references: GDB:120082; OMIM:147370
C:Map position: 15q26.1-15qter
C:Complex: heterotetramer of 2 alpha and 2 beta chains: alpha and beta chains are derivative of the same gene
C:Disulfide bonds: the two alpha chains are disulfide bonded; also naturally forms a disulfide bonded hybrid
C:Function:
A:Description: membrane glycoprotein that mediates the effects of insulin-like growth hormone (IGF) on growth and differentiation
C:Superfamily: Insulin receptor; protein kinase homology
C:Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoproteolysis
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-736/Product: insulin-like growth factor 1 receptor alpha chain #status predicted <SIG>
F:1178-332/Region: cysteine-rich
F:741-1367/Product: insulin-like growth factor 1 receptor beta chain #status predicted <SIG>
F:936-958/Domain: transmembrane #status predicted <TM>
F:997-1273/Domain: protein kinase homology <KIN>
F:1005-1013/Region: protein kinase ATP-binding motif
F:1029_135_244_314_417_438_534_607_622_640_756_764_900_913/Binding site: carbohydrate (Asn) #status predicted
F:455-468/Disulfide bonds: #status predicted
F:544/Disulfide bonds: interchain #status predicted
F:747/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:1033_1135/Active site: Lys, Asp #status predicted
F:1161_1165_1166_1346/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

```

Query Match          9.8%: Score 346.5: DB 1: Length 1367;
Best Local Similarity 27.9%: Pred. Matches 4.3e-09;
Matches 117; Conservative 64; Mismatches 147; Indels 91; Gaps 18;

OY 20 SAELDSGGFGKV-----SLCFHRTGGLMKTQYVKGKNCIEHNEALLEAKMNRLRHS 73
Db 1002 SRELGQSGFQWYEGVAKGVYKDEPETRVAIKTVNMAASMERIE-FLNEASVYKFNCH 1060

OY 74 RYVALLGVIIEGGKYSLVMEYMEKGNL--MHVYKAEMS-----TPLSVKRITLL--EIT 123
Db 1061 HAVRLRLGVSGGQPTVLIMELMTRGDLKSYLRSLRPENNNPVLAPPSLSKIMIDAGETA 1120

OY 124 EGMGYELHGKGVYIHKDLPENILVNDNFHRIADLGLASFKMKSKLNNENHNELEQVGTGA 183
Db 1121 DGMAYLVANKRVYHNDLARNCMVAEDFTYKIGDGM-----RDITYDYRR 1167

OY 184 KKGNGTL--YYADPEHLNDVNAKPTKESDYVSFAVVLMAIFA-NKEPYENAIICEQOLIMC 240
Db 1168 KGGKGLLPVRRMSPSESLKD--GVFTTYSDDVVSFQVVLMEITTLAEOPQGLSNEQVLRV 1225

OY 241 IKSG--NRPDVDDITEYQPRELISLMLKWCWANGEARPTFGCIEKKRPFTLSQLESYE 298
Db 1226 MEGGLLDKPD-----NCPDMLFELMRKQWYNKMRSPLET-----ISSIKDEME 1271

OY 299 EDVKSLLKXESNENAV-----VKRMOSLQDCVAVPSSRSNSATTEQGLSHSSQGL 349
Db 1272 PGFREVSYFYSEEKRLPEPELDELEPENMESVPLD-----PSASSSSLPLP-DRHSGH- 1323

OY 350 GMGVVEESWFAPLSEHQEENERS-----LQSKLQDEANY-HLYGSRMDRDTKQOPRON 402
Db 1324 -----KAENGPGPGVVLVLAASFDEKQPAVHAHNNQGRKNEEALPLDPOSS 1365

```

A:Residues: 1467 <RES>
A:Cross-references: GB:L34542; MID:g530137; PIDN:AAA64524.1; PID:g530158
C:Genetics:
C:Gene: batk
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F.14-64/Domain: SH3 homology <SH3>
F.181-170/Domain: SH2 homology <SH2>
F.192-445/Domain: protein kinase homology <KIN>
F.200-208/Region: protein kinase ATP-binding motif

Query Match	3.7%	Score 343;	DB 2;	length 467;
Best Local Similarity	33.2%	Pred. No. 1,8e-09;		
Matches	89;	Conservative	47;	Mismatches 100; Indels 32; Gaps 9;
QY	21	AELDSGGGKSLCNRHTQGLMT-MKTYKKGPCNTEHNEALLLEAKKMINRLRHSKVALL	79	
DB	198	AOIGEGEGAAV-----DQGYLGGKAVVAKIKKCSVTQAQELDEFAVTKLKQHRNLVLL	251	
QY	80	GVIIIEEGKYSLVMEYMERGNLMHVKAKSMRPLSVKGV--RIILEIIEGMCYLHGKGVILK	137	
DB	252	GVILLHGLY-LVMEHVSKGNLVNLFRTRGRALVSYSLQDLQALHVAEGEMETLESKVLVHR	310	
QY	138	DLKRPNILLVNDNFHKINDGLGLASKKMKMSKILNNEHNLREYDGAKKNGSTLYYMAEEN	197	
DB	311	DLAARNILLVSDGLVAKVSDPGLAKELKKGLDSSRL-----PVKWTAEBA	355	
QY	198	LDNVAKPTEKSDVYSFAVNLMAIFA-KREPEYENAIICEQOLIMCIKSNRPDVDDITTEYC	256	
DB	356	LK--NGRRSSASDVMSFCVGLLMEVPSYGRAPYPK-MSLKEVSEANKEKGYRMEPPD---SC	409	
QY	257	PREIISLKLCLNEANPEARPTTFPGLEEK	284	
DB	410	PGVYHTLMGSCWEAEPSRRPRPKIYER	437	

RESULT 4
156579
Protein-tyrosine kinase (EC 2.7.1.112) batk - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Mar-2000
C:Accession: 156579
R:Kuo, S.S.; Moran, P.; Griep, J.; Armanini, M.; Phillips, H.S.; Goddard, A.; Caras, I.W.
J. Neurosci. Res. 38, 705-715, 1994
A:Title: Identification and characterization of Batk, a predominantly brain-specific non-
A:Reference number: 156579; PMID:95106341; PMID:7807586
A:Accession: 156579
A:status: preliminary; translated from GR/EMBL/DBD
A:Molecule type: DNA

```

QY 20 SAELDSGCFGV-----SLCFHRTQGLMKTYYKGCNLEIHNALLLEAKKMMNRLHS 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 SRELGGSGFGWYEGVAGVYKDEPETFVALIKTVLEAASMERIE--FLNEASVYKFEFNCH 333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 RVVRLKGLTIEEGKSLIVMEYMEKGNL---NHVLKAEAS-----TPLSVKRITLL--ELI 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 334 HVVRLLGVSOGQPLVLMETMTRKDELQSYRSLRPEKENNPVLAPSLSKMIDWAGETA 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 124 GGMCTLLKSGVJHKDKLPENTLVNDFFHKLADIADLSFKKMSKLNNEHNHMLREVDSFTA 183
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 394 DGMATLVNANKRVHRLAARNCMVAEDFYVKIGDGMT-----RDITYETDYYR 440
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 KKNGGTL--YYMAPEHLNDVNAKPTKESDVYSFAVVLMAIFA--NKEPYENALICEOOLIMC 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 441 KGGKILLYRWMSPESLKD--GVFTTHSDVMSFGVYLWEIATLADQPYOGLSNEQVLRV 498
 QY 241 IKSG--NRPDVDITTEYCPREIISLMKLCWENANPARPTFIEKFRFYISQLEESVE 298
 Db 499 MEGGILLDPD-----NCPDMLFELMRMCWOYNPKMRPSFLEI-----ISSVKDME 544
 QY 299 EDVKSILKREYSNENAVVRMOSIQDCAVPSRSNSATTEQPSLHSSQGLQMGPEESW 358
 Db 545 AGFREVSFYSEEN---KPEPEELDL-----EPENNESV-----PLDPSA 582
 QY 359 FAPSLIEHP-----QEENEPS-----LOSKLODEANY-HLYGSRMDROTKOOPRON 402
 Db 583 SSASLPLDRHSGHKAENGPGGYLVLRASPEDERQYAHMNGRKRENERALPLPOSS 638

RESULT 6

T20082

Hypothetical protein F33E2.2 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T20082; T21703

R:Lennard, N.

Submitted to the EMBL Data Library, April 1998

A:Reference number: Z19221

A:Accession: T20082

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-855 <MW1>

A:CROSS-references: EMBL:AL022593; PIDN:CA118635.2; GSPDB:GN00019; CESP:F33E2.2

A:Experimental source: clone C49G9

A:Reference number: Z19461

A:Accession: T21703

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-855 <MW2>

A:CROSS-references: EMBL:284574; PIDN:CA806544.2; GSPDB:GN00019; CESP:F33E2.2

A:Experimental source: clone F33E2

C:Genetics:

A:Gene: CESP:F33E2.2

A:Map position: 1

A:Introns: 47/2; 213/2; 263/2; 366/3; 494/1; 547/3; 608/1; 826/3

Query Match 9.6%; Score 340.5; DB 2; Length 855;
 Best Local Similarity 22.9%; Pred. No. 4.8e-09;
 Matches 162; Conservative 94; Mismatches 259; Indels 191; Gaps 28;

QY 13 KSSD-----FLESALDSGGFGKVSICFHRTOGLMTKTVYKGPNCIEHNEALLE-EAK 65
 Db 49 KSEDELWEIPDAISELEMLGSGGAGV---RCOLENRVY-----AVKKNQKETEIK 100
 QY 66 MNNRLRSRRVYKLLGVIIEEGKYSILVMEYMEKGNIMHYLKAEMSTPLSVKRILLETIEG 125
 Db 101 HLRHLRHONITETFGVSCSPCYCTVMEYCSKGLCYLAKSRNTITRELFAPQWKEIADG 160
 QY 126 MCVLHGKGVTHKDKLPENITLVNDPFHRIADIGLASEFKWMSKLNNHEHNELEVDGTAKK 185
 Db 161 MHYHLHOKVTHIRDLSKPSNILLSAEDSTIKICDFTSHNQ-----KKKDSITMS 207
 QY 186 NGGLTYAPRHLNDVNAPK-TEKSDVYSFAVVLMAIFANKPEYMAICEQOLIMCISKG 244
 Db 208 FCGGVSMWAPEM---IKKPCNEKVDVYSFGVVLMEMLTRETPEYAN-IAQVAIIFGVGTN 263
 QY 245 --NRPDVDITTEYCPREIISLMKLCWENANPARPTFIEK---EKFRFYISQLEE----- 295
 Db 264 ILSLP-----MPEAPKGLVILIKQCLSQKGRNRSFSHIROHWEIIFKPELFEMTEEMOL 319
 QY 296 -----SVEEDVKSILKREYSNENAVVRMOSIQDCAVPSRSNSATTEQPSLHSSQGLQMGPEESW 358
 Db 320 AMSDYREFAKCIQYPTVTRDGHGPKSAFMAEEIQRKHEDQLNHIDIRIMYEMKL--- 376

QY 327 AVPSRSNSATTEQPSLHSSQGLQMGPEESWFAPSLEHPQDENPSSLQKLODEANYHL 386
 Db 377 ---KRTKMKDKLOGCTTEIKLKESELA-EWEDLTEREOMHNONSKAAVAPRAQIRG 431
 QY 387 YGSR---MDROTQOPRONAYVN-REEERRRRVSHDPAQORPEYENFQNTGKGYVSS 441
 Db 432 YPNEGIDMDSDEDDQPCRGSPYRCSTNTSSSGVSSPFSHQ---SSRSRSGAQOTRSE 488
 QY 442 AA-----SHGNAVHPSSLTS----- 457
 Db 489 GANPKILRNDALIRHSGSYWETLGARGSPARDGFSODSGMWSAGASCTAINGGQOV 548
 QY 458 -QPVLYXON-NGLYSSHEFGTR-----PLDGTGTA--GPRVY-PRIPSHMPLNINI--P 504
 Db 549 CYSOTLYRNGDGRNSDGRFIASRRVSVYVKNSTAVPQGPVFTTDSRRVY--HGVISCS 606
 QY 505 VPETNYLGNPTMPRESSLP-----PTDESIKTYTNSGTGIGTIGAYNMEIG 550
 Db 607 SPRSSSKLRNSYSFRNAPHOLEDGCCAHARAPRAKSIAYPM----- 649
 QY 551 GTSSSLDSTMTNKEEPAAYQALFDNTTSLTQKHLDPTENLCK 596
 Db 650 -TSS-----RASPPTYDNDFENAESFVDPESPRKNLKEK 685

RESULT 7

I48926

protein-tyrosine kinase (EC 2.7.1.112) CLK - mouse

N:Alternate names: csk-type protein-tyrosine kinase

C:Species: *Mus musculus* (house mouse)

C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 04-Feb-2000

C:Accession: I48926

R:Klagges, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J.B.; Penhallow, R.C.

Proc. Natl. Acad. Sci. U.S.A. 91, 2597-2601, 1994

A:Title: CLK: a protein-tyrosine kinase related to Csk that defines an enzyme family.

A:Reference number: A53469; MUID:94195789; PMID:7511815

A:Accession: I48926

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-465 <RES>

A:CROSS-references: EMBL:U05210; NID:9450232; PIDN:AA118829.1; PID:9450233

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F:13-63/Domain: SH3 homology <SH3>

F:80-169/Domain: SH2 homology <SH2>

F:191-443/Domain: protein kinase homology <KIN>

F:195-207/Region: protein kinase ATP-binding motif

Query Match 9.5%; Score 338.5; DB 2; Length 465;
 Best Local Similarity 33.6%; Pred. No. 3e-09;
 Matches 90; Conservative 46; Mismatches 99; Indels 33; Gaps 10;

QY 21 AELDSGGFGKVSICFHRTOGLMT-MKTVYKGPNCIEHNEALLEAKMMNRLRSRVYKL 79
 Db 197 AQIEGEGFAGV-----LQGEYLQKVAVNKICKDVTQAQFLEDTAVMTKLQHNELVRL 250
 QY 80 GVIIIEGKYSILVMEYMEKGNIMHYLKAEMSTPLSVK-RIIEIIEGMCYILGKGYIHK 137
 Db 251 GVILHGLY-IVMHVYSKGNLVNLFRTGRALVYSTQLOLPAHVAAGMGLSKLVHR 309
 QY 138 DLKPEITLVNDPFHRIADIGLASEFKWMSKLNNHEHNELEVDGTAKKNGTLYYNAPEH 197
 Db 310 DLARNITLVSHDLVAKVSDGLK-----AERGGIDSSRL-----PVKWTAPRA 353
 QY 198 LNDVNAPTEKSDVYSFAVVLMAIFA-NKEPYENALCEQOLIMCISGNRPDVIDITEYC 256
 Db 354 LK--NGRESSKSDVMSFGVVLMEYFSGYGRAPYK-MSLKEVSAVEKGYRMEPPD--GC 407
 QY 257 PREIISLMKLCWENANPARPTFIEK 284
 Db 408 PGSVHTLMGSCWEAPRRPPRKIVK 435

RESULT 8

159296

protein-tyrosine kinase (EC 2.7.1.112), megakaryocyte-associated - mouse

N:Alternate names: ctk

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 04-Feb-2000

C:Accession: 159296; 159807; B55625; 149621

R:Chow, L.M.L.; Jarvis, C.D.; Hu, Q.; Nye, S.H.; Gervais, F.G.; Velllette, A.; Mattis, L. Proc. Natl. Acad. Sci. U.S.A. 91, 4975-4979, 1994

A:Title: Ntk: A Csk-related protein-tyrosine kinase expressed in brain and T lymphocytes

A:Reference number: 159296; MUID:94255451; PMID:8197166

A:Accession: 159296

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-505 <RES>

R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C. Oncogene 9, 3437-3448, 1994

A:Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine prote

A:Reference number: 158407; MUID:95060800; PMID:7970703

A:Accession: 158407

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-43 <RES>

A:Cross-references: GB:I33339; NID:g609536; PIDs:AAA64431.1; PID:g609537

R:Avraham, S.; Ujang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avraham, J. Biol. Chem. 270, 1833-1842, 1995

A:Title: Structural and functional studies of the intracellular tyrosine kinase MATK ge

A:Reference number: A55625; MUID:95130565; PMID:7530249

A:Accession: B55625

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 41-505 <AVR>

R:Kaneko, Y.; Nonoguchi, K.; Fukuyama, H.; Takano, S.; Higashitsuji, H.; Nishiyama, H.; Oncogene 10, 945-952, 1995

A:Title: Presence of alternative 5' untranslated sequences and identification of cells e

A:Reference number: 149621; MUID:95206787; PMID:7898936

A:Accession: 149621

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 41-505 <RES>

A:Cross-references: GB:DA5243; NID:g639858; PIDs:BA081199.1; PID:g639858

C:Genetics:

A:Gene: Ntk; p56nck

A:Introns: 23/3

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F:53-103/Domain: SH3 homology <SH3>

F:120-209/Domain: SH2 homology <SH2>

F:231-483/Domain: protein kinase homology <KIN>

F:239-247/Region: protein kinase ATP-binding motif

Query Match 9.5%; Score 338.5; DB 2; Length 505;

Best Local Similarity 33.6%; Pred. No. 3.3e-09;

Matches 90; Conservative 46; Mismatches 99; Indels 33; Gaps 10;

21 AELDSGGFGKYSLCFHTQTGLMI-MKTYVKGPNCTIENHALLLEAKMMNRRLRHSRYVLL 79

237 AQIGGEGGAV-----LQGEYLGQKAVKVIKICDVTQAPLDFEAVVTKLQHNILVRL 290

80 GYIIEGKYSILVMEEMEGNIMHVLKADMSPLSYKG--RIILLEIISGMYLHGKGYIHK 137

291 GYIILHGLY-IVMEHVSQGNLVNPLRTGRALVSYSQLQPLAHVAEGMELESKKIIVR 349

138 DLKPNILVNDMFHTIKINDGLASFKMWSKLNNEHNLELRVDGAKNGSTLYVMAPEH 197

350 DLAAANILVSEDLVAKVSDFGIAK-----AEKGLDSSRL---PVKWTAPEA 393

198 LNDVNAKPTKSDVYSFAVNVLMIFA-NKEPYENAIQOOLIMCIKSGNRPDVDITPYC 256

394 LK-NGRRSSKSDVMSFVLLMEVYSYGRAPYPR-MSLKEVSEAVENKGYRMEPPD--GC 447

257 PREITSLMKLCLEANPEARPTTPPGIEEK 264

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Db      448  PGSVHTLMGSCHEAPRRPFKRIVER  475
RESULT 9
A33837
Insulin-like growth factor I receptor precursor - rat
N:Contains: insulin-like growth factor I alpha chain; insulin-like growth factor I beta
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Mar-1990 #sequence Revision 03-Nov-1995 #text change 21-Jul-2000
C:Accession: JC2461; A33837; PC1131
R:Pedini, M.T.; Giorgio, F.; Smith, R.J.
Biochem. Biophys. Res. Commun. 202, 1038-1046, 1994
A:Title: cDNA cloning of the rat IGF I receptor: Structural analysis of rat and human
A:Reference number: JC2461; MUID:94324926; PMID:8048916
A:Accession: JC2461
A:Molecule type: mRNA
A:Residues: 1-1371 <PED>
R:Werner, H.; Woloschak, M.; Adamo, M.; Shen-Orr, Z.; Roberts Jr., C.T.; Leroith, D.
Proc. Natl. Acad. Sci. U.S.A. 86, 7451-7455, 1989
A:Title: Developmental regulation of the rat insulin-like growth factor I receptor gene
A:Reference number: A33837; MUID:90017496; PMID:2477843
A:Accession: A33837
A:Molecule type: mRNA
A:Residues: 1-364 <WER>
A:Cross-references: GB:M27293
R:Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.
Biochem. Biophys. Res. Commun. 187, 934-939, 1992
A:Title: A new member of the insulin receptor family, insulin receptor-related receptor
A:Reference number: PC1130; MUID:92412145; PMID:1530648
A:Accession: PC1131
A:Molecule type: mRNA
A:Residues: 913-984, 'PY', 987-1017 <KUR>
A:Cross-references: GB:D12679; NID:9220918; PID:BA20983.1; PID:g4433359
C:Superfamily: Insulin receptor; protein kinase homology
C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; transmembrane
F:31-741/Domain: signal sequence #status predicted <SIG>
F:71-741/Product: insulin-like growth factor I alpha chain #status predicted <IGA>
F:742-1371/Product: insulin-like growth factor I beta chain #status predicted <IGB>
F:937-959/Domain: transmembrane #status predicted <TM>
F:971-974/Region: GPX motif
F:978-981/Region: NPX motif
F:998-1275/Domain: protein kinase ATP-binding motif
F:1006-1014/Region: protein kinase ATP-binding motif

Query Match      9.5%; Score 338; DB 2; Length 1371;
Best Local Similarity 27.2%; Pcore No.1,1e-08;
Matches 115; Conservative 65; Mismatches 143; Indels 100; Gaps 19;

Qy      22  ELDSGPFKVV-----SLCFHRTQGLMTKTVYKGPNCIEHNEALLBEAKMNRRLRSRV  75
Db      1005  ELGGGSGFMYVEGVAKGVKDEPETRVAIKTVNEAASRREIE-FLNDAASYMKFENCHV  1063

Qy      76  VLLGVITIEEGKYSLSVMEYMERGNLMHVLKA-----EMSTPLSVKGRITL  120
Db      1064  VLLGVVSGQPTVIMELMTLRGLDKLSYLSRLPEVEEQNNLVLIIPPSLSKMIQAG----  1119

Qy      121  EIEEMCVLHGCVGHKRLKRPENILVNDPFIKADIADGLAFKMKSKLNNEHNEHLREVD  180
Db      1120  ETDADMALVLANKEFVHRLAARNCVAVADPFVKIGDFQW-----RDITYETD  1166

Qy      181  GTAKKNGGTL--YYWAPHLNDVNAKPTKSDVYSFAVLVAIFA-NKEPYENAIQFOOL  237
Db      1167  YRRKGGKRLPLVRRMSPSLKD--GVFTTHSDVNSFGVLMELINTLAEQPTQGSNDEVL  1224

Qy      238  IMCISKG--NRPDVDDITEYCPREILISLMKLWEANPEARPTF---PGIEKFRP----  287
Db      1225  RFVMEGGLDLPD-----NCPDMLFELMRMCWOYVNPMPKRSFLEIIGSISIDEMEPSFOE  1278

Qy      288  --FYLSQLEESVEEDVYKSLKKEYSNNMVAVRMOSLDQCAVVASRSNSATTEQPGSLHS  345
Db      1279  VSFYISENNKPEPEDELMLELEPEN-----MSVVPD-----PSASSASL-----  1320

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OY 346 SOGLGMPVEESWEPDLEHP--QEEENEPS---10SKL0DEANY-HLVGSRMDROTQOP 399
Db 1321 -----PLPE-----RHSGHKAENGCVLVLTRASPDROPYAMNNGRANERRLPLP 1366
OY 400 RON 402
Db 1367 QSS 1369

RESULT 10

A55625
protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form - human
M:Alternate names: hematopoietic consensus tyrosine-lacking (HYL) non-receptor tyrosine
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 26-May-2000
C:Accession: A55625; S45533; 158397; T46323
R:Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L.L.; White, R.A.; Avraham,
J. Biol. Chem. 270, 1833-1842, 1995
A:Title: Structural and functional studies of the intracellular tyrosine kinase MATK ger
A:Reference number: A55625; MUID:95130565; PMID:7530249
A:Accession: A55625
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-507 <AVR>
A:Cross-references: GB:S75164; NID:9896217; PIDN:AC60645.1; PID:9896220
R:Sakano, S.; Iwama, A.; Inazawa, J.; Ariyama, T.; Ohno, M.; Suda, T.
Oncogene 9, 1155-1161, 1994
A:Title: Molecular cloning of a novel non-receptor tyrosine kinase, HYL (hematopoietic
A:Reference number: S45533; MUID:94181267; PMID:1341117
A:Accession: S45533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-507 <SAK>
A:Cross-references: EMBL:X77278; NID:9471312; PIDN:CA54493.1; PID:9557272
R:McVicar, D.W.; Lal, B.K.; Lloyd, A.; Kawamura, M.; Chen, Y.Q.; Zhang, X.; Staples, J.E
Oncogene 9, 2037-2044, 1994
A:Title: Molecular cloning of 1sk, a carboxyl-terminal src kinase (csk) related gene, ex
A:Reference number: 158397; MUID:94268844; PMID:7516063
A:Accession: 158397
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 42-149, 'GG', 152-160, 'T', 162-288, 'C', 261-296, 'D', 298-336, 'R', 338-362, 'E', 364-
A:Cross-references: GB:S71669; NID:9555593; PIDN:AA30995.1; PID:9559594
R:Duesterhoft, A.; Lauber, J.; Mewes, H.W.; Well, B.; Wiemann, S.
Submitted to the Protein Sequence Database, January 2000
A:Reference number: 223036
A:Accession: T46323
A:Molecule type: mRNA
A:Residues: 'GNGATPSSKCSRDRLGVCRLAEALLGAGAGSGCAPPCQ', 25-507 <AAA>
A:Cross-references: EMBL:AL137754
A:Experimental source: adult testis; clone DKFZp434N1212
C:Comment: For an alternative splice form, see PIR:A49865.
C:Genetics:
A:Gene: GDB:MATK; 1sk
A:Cross-references: GDB:304667
A:Map position: 19p13.3-19p13.3
A>Note: DKFZp434N1212.1
C:Superfamily: protein-tyrosine kinase src; protein kinase homology: SH2 homology: SH3
F:55-105/Domain: SH3 homology <SH3>
F:123-211/Domain: SH3 homology <SH3>
F:233-485/Domain: SH2 homology <SH2>
F:241-249/Region: protein kinase homology <KIN>
F:241-249/Region: protein kinase ATP-binding motif

Query Match 9.5%; Score 337.5; DB 2; Length 507;
Best Local Similarity 32.6%; Pred. No. 3.7e-09;
Matches 90; Conservative 47; Mismatches 90; Indels 49; Gaps 11;

OY 21 AELDSGGFGKYSLCFHRTOGLMI-MKTVYKGPNCIEHNEALLLEAKMNLRLHRSRYVLL 79
Db 239 AOIGEGGAV-----LQGEYLGQKVAVKNIKCDVNAQAFDLDETAVMTKKQHENVRL 292

OY 80 GVIIERGKSYLMEYMEKGNLMHVLAKEMSTPLSVKGRIT-----LETIEGMYL 129
Db 293 GVILHNGLY-IMYEHVSKNLVNFLE-----TRGALVTAQDLQSLHVAAGMYL 343
OY 130 HGKGVILHNDKPELILVNDNFHRIKADGLASFMMKSKLNNEHNELEVDGTAKNGT 189
Db 344 ESKKLVHRDLAARNLILVSEDLVAKVSDFLAK-----AEKGDLSSRL-----P 387
OY 190 LYVMAPEHLNDVNAKPTESDYVSFAVYLMALFA-NKEPYENATEOOLIMCIGKSNPD 248
Db 388 VKMTAPEALK--HGFTSKSDVWSFGVLLMEVFSYGRAPYK-MSLKEVSEAVEKGYRME 444
OY 249 VDDITEYCPRETIISLMKLCWEANPEARPFPGIEEK 284
Db 445 P---PEGCGPQHVLMSSQWEAPARRPRFKLAEK 477

RESULT 11

B87950
protein F33E2.2 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: B87950
R:anonymus, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/95C/C_elegans/ and www.sanger.ac.uk/projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: B87950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-848 <STO>
A:Cross-references: GB:chr_I; PIDN:CAB06544.1; PID:93876653; GSPDB:GN00019; CESP:F33E
C:Genetics:
A:Gene: F33E2.2
A:Map position: 1

Query Match 9.5%; Score 336.5; DB 2; Length 848;
Best Local Similarity 24.8%; Pred. No. 7.4e-09;
Matches 127; Conservative 75; Mismatches 206; Indels 105; Gaps 18;

OY 13 KSSD-----FLESALDSGGFGKYSLCFHRTOGLMIKTVYKGPNCIEHNEALL-EAK 65
Db 49 KSEDELWEIPDPAISELEWLGSGGAYF---RQLENRIV-----AVKKNOJLKEIPIK 100
OY 66 MNNLRHRSRVYKLLGVITIEEYKSYLMEYMEKGNLMHVLAKEMSTPLSVKGRITILETEG 125
Db 101 HLRLHONILIEFLGVCSPCYCIYMEYCSKGLCTVLCASRNITITRELFQOWKETADG 160
OY 126 MCVLHGKGVIRKDKPENIILVNDNFHRIKADGLASFMMKSKLNNEHNELEVDGTAKK 185
Db 161 MHYLLHOKVIRHDLKSPNIIISAEISTIKCDFGSHMO-----KKMDSTWMS 207
OY 186 NGTLTYMAPRHLNDVNAKP--TEKSDVYSFAVYLMATFANKPEYENALICEOOLIMCIRSG 244
Db 208 FCGTVSWMAPEM---IKKQPCNEKVDVYSFEGVILMEMLITRETPYAN-IAQMAIIIEGCTN 263
OY 245 --NRPDVDDITEYCPRETIISLMKLCWEANPEARPFPGIE---EKRPFYISOLEE--- 295
Db 264 ILSLP---MPEAPKGLVILIKOCLSQKGRNRPSPSHIRQHWIRFPELFEWTEEMQL 319
OY 296 -----SVEEYKSLKREYSNEMNVVYRMOSLOLDCV 326
Db 320 AMDSYREFACIQPTVYTRDGHGPKSAFAWEDEIQKRRIHDLHINDIRNMVEMKL--- 376
OY 327 AVPSRSNSATQDPGSLHSSQGLGMPVEESWEPASLEHPOEENPSLOSKLDEAYVHL 386
Db 377 ---KRTNKMKDKLQGGFTTELKKESELAE-WEWDLTEROMHONNSPKVAAPRAOLRG 431
OY 387 YGSR---MDROTQOPRONAVYN-REERRRRYSHDPFAOQRPYENFONTEKGTVYSS 441
Db 432 YPNEGIDMSSDEEDVQPCRGSPYRCNSTSSSGVQSSPFSROS-----SS 476

R:Wang, Y.

submitted to the EMBL Data Library, May 1997

A:Reference number: Z16016

A:Accession: T07406

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-829 <MAN>

A:Cross-references: EMBL:Y13273; NID:e1050452; PIDN:CAA73722.1; PID:e34294

A:Experimental source: strain UC82B; sub_species Mill

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 9.4%; Score 335; DB 2; Length 829;

Best Local Similarity 29.7%; Pred. No. 8.5e-09;

Matches 92; Conservative 63; Mismatches 123; Indels 32; Gaps 11;

QY 4 DMSLWIKMSSDFLESALDGGFGVSLCFHRTQ---GLIMKTYKKGNCIEHNAL 60
 Db 542 DLVEEFNIPWNLILMEKIGAGSFGV---HRGDMHGSVAVKILMEODFAERKEF 597
 QY 61 LEEAKMNNRLRHSNVVLLVYIEEGYSLVMEYMEKGNLMHVL-KAEMSTPLSVKGRRI 119
 Db 598 LREVALMKRLRHPVIVLEMGAVIOPNLSITETVLSGSLYRLLRKRGAREVDERRRLLC 657
 QY 120 L-EIEGMCYLHGKG--VIHKDLKPNILVNDNFHKKIADLGLASFMMSKLNNEEHN 175
 Db 658 MAYDVANGMYLHKRNPPIVHRDLKSPNLLVDKKYIVKIDFGLSRKANTFL----- 710
 QY 176 LREVDGTAKKNGSTLYYMAPEHNDVNAKPT-EKSDVYSFAVYLMATFAKPEYENACE 234
 Db 711 -----SSKYAAGTPEMAPEVIRD--EPSNKSVDVSGVILMELATLQOQW-NKLN 760
 QY 235 QOLIMCISGNRPVDVDTITFCPREIISLMKLCWEANPEARPTFGIEKFRPFYLSOLE 294
 Db 761 POYIAAV-GFNRRRLDIPSDLN-QVAIIIEACMANEPMKRPFSFTIMDLRPHLKSPLP 818
 QY 295 ESYEDDVKS 304
 Db 819 PGHTDMQLL 828

RESULT 15

S49313

protein kinase - slime mold (*Dictyostelium discoideum*)C:Species: *Dictyostelium discoideum*

C>Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 24-Sep-1999

C:Accession: S52076; S49313

R:Wetterauer, B.W.; Hamker, U.; von Haeseler, A.; MacMilliams, H.K.; Simon, M.N.; Veron, Biochem. Biophys. Acta 1265, 97-101, 1995

A:Title: A protein kinase from *Dictyostelium discoideum* with an unusual acidic repeat do

A:Reference number: S52076; MUID:95161460; PMID:7857991

A:Accession: S52076

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1094 <WE2>

A:Cross-references: EMBL:Z37981; NID:9551445; PIDN:CAA86053.1; PID:9551446

C:Genetics:

A:Introns: 35/3; 104/1; 166/2

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C:Keywords: ATP

F:20-281/Domain: protein kinase homology <KIN>

F:28-36/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 9.4%; Score 334.5; DB 2; Length 1094;

Matches 123; Conservative 84; Mismatches 167; Indels 173; Gaps 20;

QY 10 IKMSSDFLESALDGGFGVSLCFHRTQGLIMKTYKKG-----PNCIE 55
 Db 17 IKYEDDFI--SELGSGGFGKV-----FKGEYLGAPVAIKKIHILLPDDPNRVD 62
 QY 56 HNEALLLEAKMNNRLRHSNVVLLVYIEEGYSLVMEYMEKGNLMHVLKAE-MSTPLSV 114
 Db 63 LKFLNREIETIKLFTHPNVIQFVGISENNCLIFIVTELLIEGDLQYLLKNQSIDLPWFL 122

QY 115 KGRITLLETIGMCYLHGKGVTHKDKLPENILVNDNFHKKIADLGLASFMMSKLNNEHN 174
 Db 123 RANILADVSLAMSYLHRSKSIYHRDLKSTNLLVDKMKIKVODFGFA-----RIVEEDNN 176
 QY 175 ELREVDGTAKKNGSTLYYMAPEHNDVNAKPTFKSDVYSFAVYLMATFAKPE----- 227
 Db 177 KSMITCGIDN-----WMSPEMTTGLD--DEKSDIFSFGIVLEILISRVKPAFAYMRDA 227
 QY 228 ---YENALCEQOLIMCISGNRPVDVDTITFCPREIISLMKLCWEANPEARPTFGIEK 284
 Db 228 SFGLAEDIVRNQL-----IPTCPESLIDLTITNCCSVDPNNRPSFEKLSQT 273
 QY 285 FRPFYLSOLESVED-----VSKLKEYSNEAV 314
 Db 274 ---LKOIKTTLDSNIVYPEIRDFEQOKISTTNGNKKQNGAPKINNLPLOYSNNNN 328
 QY 315 V-----KRMQSLQDLQVAVPSSRSNSATPEQSLHSSQGLGMPVEES 357
 Db 329 IYDDDDDDDDDDNDSEFPREYS-----DNSNSVVTLESNSNSNSTINGEQEQEQ 380
 QY 358 WFAFSLHPQEEHPSLQSLQDEANYHLYGS-----RMDROTQO---PRON 402
 Db 381 EQOQOQOQVKEERDEGELE---QDDNIEVYDSIQKLEHOKELLERONQOEGSTDEN 437
 QY 403 VAYNKEER-----RRVYS--HDPFAQRPY-----ENFQTEGKQTV 439
 Db 438 EYVEQEEEBEEDDEEQVISTPAKKRISFGODTFHVEAVRTDDEDDDEDEBEDEDE 497
 QY 440 SSAASHG 446
 Db 498 ----DHG 500

Search completed: June 21, 2003, 16:15:38
 Job time: 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 21, 2003, 15:51:05 ; Search time 26 Seconds
(Without alignments)
1070.408 Million cell updates/sec

Title: US-09-981-397a-16

Perfect score: 3545
Sequence: 1 MOPDMSLWIKMKSSDFLES.....ALHQCNRIDLLSLIYVSON 671

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3545	100.0	671	RIK1_HUMAN	Q13546 homo sapien
2	2423.5	68.4	656	RIK1_MOUSE	O60855 mus musculu
3	423	11.9	518	RIK3_HUMAN	O95722 homo sapien
4	404.5	11.4	478	RIK3_RAT	O92255 ratus norv
5	401.5	11.3	486	RIK3_MOUSE	O99210 mus musculu
6	374	10.6	539	RIK2_MOUSE	P88801 mus musculu
7	371	10.5	540	RIK2_HUMAN	O43353 h receptor-
8	370.5	10.5	832	ANR3_HUMAN	P57078 homo sapien
9	346.5	9.8	1367	IGIR_HUMAN	P80869 homo sapien
10	343	9.7	640	MATK_RAT	P41243 ratus norv
11	342.5	9.7	640	IGIR_BOVIN	O05688 bos taurus
12	339.5	9.6	1370	IGIR_RAT	P24062 ratus norv
13	338.5	9.5	505	MATK_MOUSE	P41242 mus musculu
14	338	9.5	1373	IGIR_MOUSE	O60751 mus musculu
15	337.5	9.4	507	MATK_HUMAN	P42679 homo sapien
16	335	9.4	511	LYN_HUMAN	P07948 homo sapien
17	333	9.4	1382	INSR_HUMAN	P06213 homo sapien
18	332.5	9.4	1372	INSR_MOUSE	P15208 mus musculu
19	330.5	9.3	1383	INSR_RAT	P15127 ratus norv
20	330	9.3	511	LYN_MOUSE	P35911 mus musculu
21	328.5	9.3	450	CSK_RAT	P32577 ratus norv
22	327.5	9.2	2146	INSR_DROME	P09208 drosophila
23	325.5	9.2	507	LCK_CHICK	P42683 gallus gall
24	325	9.2	606	MK7_HUMAN	O43318 homo sapien
25	324.5	9.2	497	SPK1_DGRT	P42687 dugesia tlg
26	323.5	9.1	450	CSK_HUMAN	P41240 homo sapien
27	322.5	9.1	579	MK7_MOUSE	O62073 mus musculu
28	322	9.1	511	LYN_RAT	O07014 ratus norv
29	322	9.1	1123	ABL1_MOUSE	P00520 mus musculu
30	322	9.1	1125	CYGS_STRPU	P16065 strongyloce
31	321.5	9.1	508	LCK_HUMAN	P06239 homo sapien
32	318	9.0	450	CSK_CHICK	P41239 gallus gall
33	317.5	9.0	450	CSK_MOUSE	P41241 mus musculu

34	316.5	8.9	504	1	HCK_MACFA	O95m30 macaca fasc
35	316.5	8.9	625	1	ITK_MOUSE	O03526 mus musculu
36	315.5	8.9	503	1	HCK_RAT	P50545 ratus norv
37	315	8.9	393	1	MK7_DROME	P83104 drosophila
38	315	8.9	1182	1	ABL2_HUMAN	P42684 homo sapien
39	313.5	8.8	1607	1	MIPR_LYMT	O25410 lymnaea sta
40	313	8.8	1300	1	IRK_MOUSE	O9w14 mus musculu
41	312.5	8.8	524	1	HCK_MOUSE	P08103 mus musculu
42	311.5	8.8	526	1	HCK_HUMAN	P08631 homo sapien
43	311	8.8	812	1	FGRL_XENLA	P22182 xenopus lae
44	311	8.8	986	1	CYGR_ARBP	P11528 arabacia pun
45	310.5	8.8	1297	1	IRR_HUMAN	P14616 homo sapien

ALIGNMENTS

RESULT 1
ID RIK1_HUMAN STANDARD; PRT; 671 AA.
AC Q13546: Q13180:
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.-)
DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)
DE (Receptor interacting protein).
GN RIK1 OR RIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=umbilical vein endothelial cells;
RX MEDLINE=96200892; PubMed=6612133;
RA Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
RT "TNF-dependent recruitment of the protein kinase RIP to the TNF
receptor-1 signaling complex.";
RL Immunity 4:367-396(1996).
RN [2]
RP REVISION TO 120.
RA Huang J., Hsu H., Baichwal V.R., Goeddel D.V.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE OF 300-671 FROM N.A.
RX MEDLINE=95277838; PubMed=7538908;
RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
RT "RIP: a novel protein containing a death domain that interacts with
Fas/Apo-1 (CD95) in yeast and causes cell death.";
RL Cell 81:513-523(1995).
CC -!- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND
INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-
DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U50062; AAC32232.1; -;
DR EMBL: U25994; AAC50137.1; -;
DR HSSP: P08631; IAD5.
DR Genew: HGNC:10019; RIKP1.
DR MIM: 603453; -;
DR InterPro: IPR000488; Death.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR004040; Srv_pkinase.

DR InterPro: IPR002290; Ser thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00531; death; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00221; STYKC; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00117; DEATH_DOMAIN; 1.
 DR Transfaser: Serine/threonine-protein kinase; ATP-binding; Apoptosis.
 KW Apoptosis.
 FT DOMAIN 17 289
 FT NP_BIND 23 31
 FT BINDING 49 49
 FT ACT_SITE 138 138
 FT DOMAIN 583 669
 FT DOMAIN 411 414
 FT CONFLICT 514 514
 FT SEQUENCE 671 AA; 75958 MW; BAD4E7E70456ABE CRC64;

Query Match 100.0%; Score 3545; DB 1; Length 671;
 Best Local Similarity 100.0%; Pred. No. 1,7e-201;
 Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOPDMSLVINIKMKSSDFLESALDSGGFGKVSICFHRTOGLIMKTGYKPCIEHNEAL 60
 DB 1 MOPDMSLVINIKMKSSDFLESALDSGGFGKVSICFHRTOGLIMKTGYKPCIEHNEAL 60
 QY 61 LEEAKMMNRLRHSRVKILGVIIIEGKYSLVMEYMEKGLMVLAKEMSTPISSVGRILL 120
 DB 61 LEEAKMMNRLRHSRVKILGVIIIEGKYSLVMEYMEKGLMVLAKEMSTPISSVGRILL 120
 QY 121 EIIIEGMYLHGKGVIIHKDLKPEIILVNDNFHRIADLGLASFKMSKLNNEENELREVD 180
 DB 121 EIIIEGMYLHGKGVIIHKDLKPEIILVNDNFHRIADLGLASFKMSKLNNEENELREVD 180
 QY 121 EIIIEGMYLHGKGVIIHKDLKPEIILVNDNFHRIADLGLASFKMSKLNNEENELREVD 180
 DB 121 EIIIEGMYLHGKGVIIHKDLKPEIILVNDNFHRIADLGLASFKMSKLNNEENELREVD 180
 QY 181 GTAKNNGCTIYMAEPEHNDVAKPTKESDVSPFVAVYMAIPANKPEPENAIICEQOLMC 240
 DB 181 GTAKNNGCTIYMAEPEHNDVAKPTKESDVSPFVAVYMAIPANKPEPENAIICEQOLMC 240
 QY 181 GTAKNNGCTIYMAEPEHNDVAKPTKESDVSPFVAVYMAIPANKPEPENAIICEQOLMC 240
 DB 181 GTAKNNGCTIYMAEPEHNDVAKPTKESDVSPFVAVYMAIPANKPEPENAIICEQOLMC 240
 QY 241 IKSGRNPVDVITTEYCPREIISLMKLCWEANPEARPTFGIIEKRPFLSOLSESVED 300
 DB 241 IKSGRNPVDVITTEYCPREIISLMKLCWEANPEARPTFGIIEKRPFLSOLSESVED 300
 QY 241 IKSGRNPVDVITTEYCPREIISLMKLCWEANPEARPTFGIIEKRPFLSOLSESVED 300
 DB 241 IKSGRNPVDVITTEYCPREIISLMKLCWEANPEARPTFGIIEKRPFLSOLSESVED 300
 QY 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEQPSGLSHSSQGLGMCPVEESMFA 360
 DB 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEQPSGLSHSSQGLGMCPVEESMFA 360
 QY 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEQPSGLSHSSQGLGMCPVEESMFA 360
 DB 301 VKSLKKEYSNENAVVKRMQSLQDCVAVPSSRSNSATEQPSGLSHSSQGLGMCPVEESMFA 360
 QY 361 PSLEHPOENEPSLOSRLQDEANVLYGSSRMDROKQPRONVAVNREERRRVSHPDF 420
 DB 361 PSLEHPOENEPSLOSRLQDEANVLYGSSRMDROKQPRONVAVNREERRRVSHPDF 420
 QY 361 PSLEHPOENEPSLOSRLQDEANVLYGSSRMDROKQPRONVAVNREERRRVSHPDF 420
 DB 361 PSLEHPOENEPSLOSRLQDEANVLYGSSRMDROKQPRONVAVNREERRRVSHPDF 420
 QY 421 AQQRPYENFQNTGEGKGVYSSAASHGNAVHOPSGILTSOPVLYONNGLYSSHGFEPLD 480
 DB 421 AQQRPYENFQNTGEGKGVYSSAASHGNAVHOPSGILTSOPVLYONNGLYSSHGFEPLD 480
 QY 421 AQQRPYENFQNTGEGKGVYSSAASHGNAVHOPSGILTSOPVLYONNGLYSSHGFEPLD 480
 DB 421 AQQRPYENFQNTGEGKGVYSSAASHGNAVHOPSGILTSOPVLYONNGLYSSHGFEPLD 480
 QY 481 PGTAGPRVWYRPIPSHMSLHNIPVETNYLGNTPTMPFSSLPPTDESIKTYIYNSTGIQ 540
 DB 481 PGTAGPRVWYRPIPSHMSLHNIPVETNYLGNTPTMPFSSLPPTDESIKTYIYNSTGIQ 540
 QY 481 PGTAGPRVWYRPIPSHMSLHNIPVETNYLGNTPTMPFSSLPPTDESIKTYIYNSTGIQ 540
 DB 481 PGTAGPRVWYRPIPSHMSLHNIPVETNYLGNTPTMPFSSLPPTDESIKTYIYNSTGIQ 540
 QY 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYQALFNDTITSLTKHLDPIRENIQKHKKN 600
 DB 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYQALFNDTITSLTKHLDPIRENIQKHKKN 600
 QY 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYQALFNDTITSLTKHLDPIRENIQKHKKN 600
 DB 541 IGAVNYMEIGTSSSLDSTNTNKEKPAKYQALFNDTITSLTKHLDPIRENIQKHKKN 600
 QY 601 CARLIGFTQSOIDEIDHYERDGLKEKYOMLOKVMVMEGIGKATVGLAALHQCSDID 660
 DB 601 CARLIGFTQSOIDEIDHYERDGLKEKYOMLOKVMVMEGIGKATVGLAALHQCSDID 660
 QY 601 CARLIGFTQSOIDEIDHYERDGLKEKYOMLOKVMVMEGIGKATVGLAALHQCSDID 660
 DB 601 CARLIGFTQSOIDEIDHYERDGLKEKYOMLOKVMVMEGIGKATVGLAALHQCSDID 660
 QY 661 LLSLLIYVSON 671
 DB 661 LLSLLIYVSON 671

RESULT 2
 ID RIK1_MOUSE
 AC 060855; STANDARD; PRT; 656 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.-)
 DE (Serine/threonine protein kinase RIP) (Cell death protein RIP)
 DE (Receptor interacting protein).
 GN RIP1 OR RIP OR RINP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RA MEDLINE=95277838; PubMed=7538908;
 RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
 RT "RIP: a novel protein containing a death domain that interacts with Fas/Apo-1 (CD95) in yeast and causes cell death.";
 RL Cell 81:513-523(1995).
 CC - FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFR1 IN A TNF-DEPENDENT PROCESS. REQUIRED FOR TNFR1 ACTIVATION OF NF-KAPPA B.
 CC - TISSUE SPECIFICITY: FOUND AT LOW LEVELS IN ALL TISSUES.
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC - SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC EMBL: U25995; AAB60487.1; -.
 DR HSSP: P25445; 1DDP.
 DR MGD: MGI:108212; Ripk1.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR004040; STY_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00531; death; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00221; STYKC; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00117; DEATH_DOMAIN; 1.
 DR Transfaser: Serine/threonine-protein kinase; ATP-binding; Apoptosis.
 KW Apoptosis.
 FT DOMAIN 17 290
 FT NP_BIND 23 31
 FT BINDING 49 49
 FT ACT_SITE 138 138
 FT DOMAIN 568 654
 FT VARIANT 473 473
 FT SEQUENCE 656 AA; 74854 MW; ABB350B523879933 CRC64;

Query Match 68.4%; Score 2423.5; DB 1; Length 656;
 Best Local Similarity 69.8%; Pred. No. 1,7e-135;
 Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

QY 1 MOPDMSLVINIKMKSSDFLESALDSGGFGKVSICFHRTOGLIMKTGYKPCIEHNEAL 60
 DB 1 MOPDMSLVINIKMKSSDFLESALDSGGFGKVSICFHRTOGLIMKTGYKPCIEHNEAL 60

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QY 61 LEAKMMNRHSHRVKLVIIIEGKSYLMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
DB 61 LEAKMMNRHSHRVKLVIIIEGKSYLMEYMEKGNLMHVLKAEKSTPLSVKGRILL 120
QY 121 EIIEMGCVLHGKGYIHKDLKPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVD 180
DB 121 EIIEMGCVLHGKGYIHKDLKPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVD 180
QY 181 GTAKK-NGTLLYMAPEHLNDVNAKPEKSDVYSFAVVLMAIFANKPEYENAIQEQLIM 239
DB 181 GTAKK-NGTLLYMAPEHLNDVNAKPEKSDVYSFAVVLMAIFANKPEYENAIQEQLIM 239
QY 240 CIKGNRPDVDDIETECREITISLMKUCMEANPEAPRPPGIEEKRPFYISQLEESVEE 299
DB 240 CIKGNRPDVDDIETECREITISLMKUCMEANPEAPRPPGIEEKRPFYISQLEESVEE 299
QY 241 CIKGNRPDVDDIETECREITISLMKUCMEANPEAPRPPGIEEKRPFYISQLEESVEE 300
DB 241 CIKGNRPDVDDIETECREITISLMKUCMEANPEAPRPPGIEEKRPFYISQLEESVEE 300
QY 300 DVSLKREYSNENAVKRMOSLQDCVAVPSSRSNATDEQSGLSHSGGLMGPEEESWF 359
DB 300 DVSLKREYSNENAVKRMOSLQDCVAVPSSRSNATDEQSGLSHSGGLMGPEEESWF 359
QY 360 APSLEHPOEENPISLOKLODEANVHYLYGSHMDROTQKOPRONVAYNEEERRRRSHDP 419
DB 360 APSLEHPOEENPISLOKLODEANVHYLYGSHMDROTQKOPRONVAYNEEERRRRSHDP 419
QY 359 SSSPEYPODENRDSVQAKLOEASVHAFGIFAEKOTKQPRQNEAYNNEEERKRKRVSHDP 418
DB 359 SSSPEYPODENRDSVQAKLOEASVHAFGIFAEKOTKQPRQNEAYNNEEERKRKRVSHDP 418
QY 420 FAQORPEENFONTEGKGTIVSSAASHGNAVHQPGLTSQPOVLYONNGLYSHGFGTRPL 479
DB 420 FAQORPEENFONTEGKGTIVSSAASHGNAVHQPGLTSQPOVLYONNGLYSHGFGTRPL 479
QY 419 FAQORPEENFONTEGKGTIVSSAASHGNAVHQPGLTSQPOVLYONNGLYSHGFGTRPL 470
DB 419 FAQORPEENFONTEGKGTIVSSAASHGNAVHQPGLTSQPOVLYONNGLYSHGFGTRPL 470
QY 480 DPGTAGRPVWRPIPSHMRSLHNPVPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVD 539
DB 480 DPGTAGRPVWRPIPSHMRSLHNPVPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVD 539
QY 471 --GTTGGVWYPPMLSQWSTYKPPVPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVD 528
DB 471 --GTTGGVWYPPMLSQWSTYKPPVPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVD 528
QY 540 QIGAVYNYMEIGTSSSLDSTNTNFKPEPAKYOAFIENFTSLDKHDIPTRENLGKHWK 599
DB 540 QIGAVYNYMEIGTSSSLDSTNTNFKPEPAKYOAFIENFTSLDKHDIPTRENLGKHWK 599
QY 529 QIGVHNTMDVGLN-----QPPNNTCKEESTSRHOAIPENTISLDEHNPITRENIGRWK 584
DB 529 QIGVHNTMDVGLN-----QPPNNTCKEESTSRHOAIPENTISLDEHNPITRENIGRWK 584
QY 600 NCARKLGFTQSQIDEIDHDERDGLKEKRYOMLQKVMREKIGATYVGLKLAQALHOCRI 659
DB 600 NCARKLGFTQSQIDEIDHDERDGLKEKRYOMLQKVMREKIGATYVGLKLAQALHOCRI 659
QY 585 NCARKLGFTQSQIDEIDHDERDGLKEKRYOMLQKVMREKIGATYVGLKLAQALHOCRI 644
DB 585 NCARKLGFTQSQIDEIDHDERDGLKEKRYOMLQKVMREKIGATYVGLKLAQALHOCRI 644
QY 660 DLSSLIYVSON 671
DB 660 DLSSLIYVSON 671
QY 645 DLNHLIRASOS 656
DB 645 DLNHLIRASOS 656

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RESULT 3

R1K3_HUMAN

STANDARD:

PRT: 518 AA.

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AC 09Y572;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 3 (EC 2.7.1.1)
DE (RIP-like protein kinase 3) (receptor-interacting protein 3) (RIP-3).
GN R1K3 OR R1P3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-50.
RC TISSUE=Cervical carcinoma; Lymphocytes;
RX MEDLINE=992872740; PubMed=10339433;
RA Yu P.W., Huang B.C.B., Shen M., Quast J., Chan E., Xu X., Nolan G.P.,
RA Payan D.G., Luo Y.,
RA "Identification of RIP3, a RIP-like kinase that activates apoptosis
RT and NF-kappaB."
RL Curr. Biol. 9:539-542(1999).
RN 12
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-50.
RC TISSUE=Fetal brain, and Aortic endothelium;
RX MEDLINE=99287880; PubMed=10358032;
RA Sun X., Lee J., Navas T., Baldwin D.T., Stewart T.A., Dixit V.M.;

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RT "RIP3, a novel apoptosis-inducing kinase.";
RL J. Biol. Chem. 274:16871-16875(1999).
CC -1- FUNCTION: Promotes apoptosis.
CC -1- SUBUNIT: Binds TRAF2 and RIP1 and is recruited to the TNF-1
CC signaling complex.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- TISSUE SPECIFICITY: Highly expressed in the pancreas. Detected at
CC lower levels in heart, placenta, lung and kidney.
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC -----
DR EMBL: AF15684; AAD39005.1; -
DR Genbank: HGNC:10021; R1P3.
DR MIM: 605817; -
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation; Apoptosis.
FT DOMAIN 21 287
FT NP_BIND 27 35 ATP (By similarity).
FT BINDING 50 50 ATP.
FT ACT_SITE 142 142 BY SIMILARITY.
FT MUTAGEN K->A: ABOLISHES KINASE ACTIVITY.
FT MUTAGEN K->D: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 518 AA; 56901 MW; 38A3ECFBBBD4151 CAC64;
Query Match 11.9%; Score 423; DB 1; Length 518;
Best Local Similarity 25.3%; Pred. No. 6.9e-18;
Matches 145; Conservative 95; Mismatches 186; Indels 146; Gaps 22;
QY 14 SDFLESSEL-DSGFGKVSCLFPHRTQGLMIMKTYVKKPCNCEIENHEALLEAKMMNRH 72
DB 14 SDFLESSEL-DSGFGKVSCLFPHRTQGLMIMKTYVKKPCNCEIENHEALLEAKMMNRH 72
QY 17 STEELNDELVGKDSFGVIFRAQHRKKG-----YDAVAIVSKAISREYKAMASLDN 69
DB 17 STEELNDELVGKDSFGVIFRAQHRKKG-----YDAVAIVSKAISREYKAMASLDN 69
QY 73 SRVYKLLGVI-----IEGKSYLMEYMEKGNLMHVLKAEKSTPLSVKGRILLIEEGMC 127
DB 73 SRVYKLLGVI-----IEGKSYLMEYMEKGNLMHVLKAEKSTPLSVKGRILLIEEGMC 127
QY 70 EFLVRLKEGVIEKVMNDQPKPALVTKFMENGLSLGLOQCPRPMPILCRLLKEVYLGMF 129
DB 70 EFLVRLKEGVIEKVMNDQPKPALVTKFMENGLSLGLOQCPRPMPILCRLLKEVYLGMF 129
QY 128 YLHGKG--VTRKDLKPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVDGTRAK- 184
DB 128 YLHGKG--VTRKDLKPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVDGTRAK- 184
QY 130 YLHQNPPVLLHRDLKPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVDGTRAK- 177
DB 130 YLHQNPPVLLHRDLKPEKNTLVNDPHIKIADGLASFQKMSKLNNEEHLREVDGTRAK- 177
QY 185 KNGGLVYMAPEHLNDVNAKPEKSDVYSFAVVLMAIFANKPEYENAIQEQLIM 236
DB 185 KNGGLVYMAPEHLNDVNAKPEKSDVYSFAVVLMAIFANKPEYENAIQEQLIM 236
QY 178 EPGGLGYLAPELFLVNVNRRKASTASDVYSFGLTMAVLAAGREVELPTEPSLYVEAVCRQ 237
DB 178 EPGGLGYLAPELFLVNVNRRKASTASDVYSFGLTMAVLAAGREVELPTEPSLYVEAVCRQ 237
QY 237 LIMCIRKSNRPDVDDIETECREITISLMKUCMEANPEAPRPPGIEEKRPFYISQLEESVEE 287
DB 237 LIMCIRKSNRPDVDDIETECREITISLMKUCMEANPEAPRPPGIEEKRPFYISQLEESVEE 287
QY 238 -----NRSLSLDELPGAGETGLEGKRLKMLQKMSSEKDKRPSQECIPKTDVETQ- 288
DB 238 -----NRSLSLDELPGAGETGLEGKRLKMLQKMSSEKDKRPSQECIPKTDVETQ- 288
QY 288 FYLSQLEESVEEDYSLKKEYSNENAVKRMOSLQDCVAVPSSRSNATDEQSGLSHSG 347
DB 288 FYLSQLEESVEEDYSLKKEYSNENAVKRMOSLQDCVAVPSSRSNATDEQSGLSHSG 347
QY 289 -----MVENNNMAASTVYDFLSQLKSSNRPE-----SIPES----- 320
DB 289 -----MVENNNMAASTVYDFLSQLKSSNRPE-----SIPES----- 320
QY 348 GLGMGPVEESWFAVSLHEPQENPISLOKLODEANVHYLYGSHMDROTQKOPRONVAYNR 407
DB 348 GLGMGPVEESWFAVSLHEPQENPISLOKLODEANVHYLYGSHMDROTQKOPRONVAYNR 407
QY 321 --GGGTGMDGFRRTIENQHSRNDVWVSEWL-----*NKLLPEPSSVPAK 365
DB 321 --GGGTGMDGFRRTIENQHSRNDVWVSEWL-----*NKLLPEPSSVPAK 365
QY 408 EERRRRVSHDPAQORPENFONTEGKGTIVSSAASHGNAVHQPGLTSQPOVLYONN 466
DB 408 EERRRRVSHDPAQORPENFONTEGKGTIVSSAASHGNAVHQPGLTSQPOVLYONN 466

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DB 366 PSILTRSRRAQEDVQVA-----WTAGTSSDSMAQP---PQTETSTERN 406
QY 467 GYSSHGFGTRPLDGTAGPRVWYRPIPSHPSLNIPIVPEINNYLGNTFMPSSLPND 526
DB 407 QMPS-----PTSTGT-----PS-----PGRNGGAEROGMMWSCTRP 441
QY 527 ESIRK---YTIYNSGTGIGIGAVNYMEIGTSS 554
DB 442 NPVTGRPLVNIYNSGVGVGDNNYLTMOQTTA 473

RESULT 4
RIK3_RAT
ID RIK3_RAT STANDARD: PRT: 478 AA.
AC Q922P5;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Receptor-interacting serine/threonine protein kinase 3 (EC 2.7.1.-)
DE (RIP-like protein kinase 3) (Receptor-interacting protein 3) (RIP-3)
DE (Homocysteine respondent protein Hcyp2).
DE RIP3 OR RIP3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar Kyoto;
RA Chen K.H., "Yang J.";
RT "A homocysteine-respondent gene cloned from WKY VSMCs by differential
RT display.";
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
CC -i- FUNCTION: Promotes apoptosis (By similarity).
CC -i- SUBUNIT: Binds TRAF2 and RIPK1 and is recruited to the TNFR-1
CC signaling complex (By similarity).
CC -i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -i- PIM: Autophosphorylated (By similarity).
CC -i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC -----
DR EMBL: AF036537; AAD02059.2; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 22 290 PROTEIN KINASE.
FT NP_BIND 28 36 ATP (BY SIMILARITY).
FT BINDING 51 51 ATP (BY SIMILARITY).
FT ACT_SITE 143 143 BY SIMILARITY.
SQ SEQUENCE 478 AA: 52234 MW: ED6C280C594E1977 CRC64;

Query Match 11.4%; Score 404.5; DB 1; Length 478;
Best Local Similarity 25.5%; Pred. No. 7.6e-17;
Matches 154; Conservative 80; Mismatches 179; Indels 191; Gaps 28;

10 IKMSSDPLES-AELDGGFGKSLCFRTGGLMTKTYVYGPNCEIENELLEAKMMN 68
I : I : I I : . : I I I I I I : I : : : : I I I

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DB 14 ISLVGSELENDLGVGKGFGAVFARHATMNLDAVAK-----IYNSKISIREVKMY 66
QY 69 RLHRSRYVALLGVILE-EEKY-----SLWEIYEKGNLHVLKAEKSTPLSYAGRIILETI 123
DB 67 NLRHENVYLLLLIGVTENLEWDYVYGPALVYGFEMENSLSLQAPSCRPPLCLRLIEVY 126
QY 124 EGMCYLH--GKGVITHDKLPENILVDNDFHITADIGLASFWMKSKLNNEHNELEVDG 181
DB 127 LGMCTYHSLNPSLHRDLKPSNVLLDLIELMAKLADFGSLTFGGSGSGS-----GS 177
QY 182 TAKKNGSTLYMAPEHLNDVNAKPTKSDVYSFAVLAIFANKP-----YENAI 233
DB 178 GSRDSGGLAYLAPE-LIDNDGKASKASDVYSFGLVMTVLGRAEVVDKTLIRGAVC 236
QY 234 EQQLIMCTKSGNRPPVDDITTECPRE-----IISLMKLCWENPPARPTFETEKFPF 288
DB 237 NRQ-----RRPPLTELPDPSPTPGIEGLKELMTQWSSEPDREPSFODCEKTNV 288
QY 289 YLSOLESEVDEEVKSLK---KEYSNENAVKRMOSIQ---LDCAVAPSSRNSATPDG 341
DB 289 YI-LVQDKVDAVSKVKHLYLSYRSSDTRKLSARESSOKTEYDC-----PRETIYEMID 342
QY 342 SLHSSQGLGMGPVEESWFAPSLEHPQENENPSLSQKLODEANYHLGSRMDRQTKQPRQ 401
DB 343 RLH-----LEEPS-----GSVPERLTSL----- 360
QY 402 NVAYNREERRRRRVSHDPAQRPPENFQNTGKGTIVSSAASHQNAHQPSGLTSQ--- 458
DB 361 -----TERRG-----KEASFGHAT--PAGTSSDTLA 384
QY 459 --PQVLYONNGLYSHGFGTRPLDGTAGPRVWYRPIPSHPSLNIPIVPEIN----- 509
DB 385 GRQQLPH-----ILPRGTTTPRAFTETEGPD-----PQRNODGRNS 422
QY 510 ---YLGNTPTMPFSSLPPTDESIKYTIYNSGTGIGAVNYMEIGTSSLLDSTNTNF-K 565
DB 423 NFWYTMNAPN-FMTGL-----QSI--VLNNKSEVQIGQHNMSV-----QPTAPPK 466
QY 566 EEPK 569
DB 467 KEPA 470

RESULT 5
RIK3_MOUSE
ID RIK3_MOUSE STANDARD: PRT: 486 AA.
AC Q9QZL0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Receptor-interacting serine/threonine protein kinase 3 (EC 2.7.1.-)
DE (RIP-like protein kinase 3) (Receptor-interacting protein 3) (RIP-3)
DE (MRIP3).
DE RIPK3 OR RIP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-143.
RC TISSUE=Embryo;
RX MEDLINE=99421935; PubMed=10490590;
RA Pazdernik N.J., Donner D.B., Goebel M.G., Harrington M.A.;
RT "Mouse receptor interacting protein 3 does not contain a caspase-
RT recruiting or a death domain but induces apoptosis and activates NF-
RT kappaB.";
RL MOL. Cell. Biol. 19:6500-6508(1999).
CC -i- FUNCTION: Promotes apoptosis.
CC -i- SUBUNIT: Binds TRAF2 and RIPK1 and is recruited to the TNFR-1
CC signaling complex (By similarity).
CC -i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -i- TISSUE SPECIFICITY: Expressed in embryo and in adult spleen,
CC liver, testis, heart, brain and lung.

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-!- PWM: Autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-----
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DR EMBL: AF178953; AAF03133.1; -.
DR MGD: MGI:2154952; Ripk3.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; kinase; 1.
DR PRINTS: PR00107; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Trnsterase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 22 292
FT NP_BIND 28 36 PROTEIN KINASE
FT BINDING 51 51 ATP (BY SIMILARITY).
FT ACT_SITE 143 143 ATP (BY SIMILARITY).
FT DOMAIN 143 143 PROBABLE.
FT MUTAGEN 153 143 PRO-RICH.
FT FT D->N: NO AUTOPHOSPHORYLATION.
SQ SEQUENCE 486 AA; 53336 MW; DD264659187D3436 CRC64;

Query Match 11.3%; Score 401.5; DB 1; Length 486;
Best Local Similarity 24.8%; Pred. 1.2e-16;
Matches 150; Conservative 87; Mismatches 191; Indels 177; Gaps 23;

OY 8 NVIKMSSDFELSAE-LDSGFGYKSLCFHRTQGLMIKITYKKGNCLEHNALLEEAKM 66
DB 12 SAVPLVSHLEELKLEFVGKGGGVFAHHRTMHDVAK-----IVNSKKSWEYKA 64
OY 67 MNRLRSHRVNVLGVILEEGRY-----SLYMEYMEKGNLMHVLKAEKSTPLSVYGRITL 120
DB 65 MVNLRNENVLLLTGV-TEDLQMDPFGSGLVTRFENENSLAGLDPEDCPRPAPLIRLLQ 123
OY 121 EIIEMCYLHG--KGVTHKDKLPENILVNDPHIKIADLGLASFEMSKLNNEHNELRE 178
DB 124 EYVLGMCAHSLDPLPLRLDLKPSNILLDPETHAKLADFGSLTFQGGSGSGSGSSGRD 183
OY 179 VDGAKKMGGLTYWAPRHLNDVNAKPREKSDVYSFAVVAIAFANKER-----YEN 230
DB 184 -----SGGLTAYLDPELKRKVNLMKASKADVYSFGLVNAVLGRARELDVKTSLIRE 236
OY 231 AICEQOLIMCKRSKRPVDDITTEYCP-----RETIISLMKLCWEANPEARPTGIEKEF 285
DB 237 TVCDRO-----SRPLTELPSQSPETPLGELKEKELMHICWGSQSENRPSPQCEPKT 288
OY 286 RPFILSQLEESVEDVYSLAKREYSNENAVVRKMSQLDCAVAPSSRSNSATEQPSLHS 345
DB 289 NEVY-NLVKDVDAVSEVKKHYLSQ-----HR 314
OY 346 SOGLGMGVESWFAFSLSEHQENEPESLQSLDDEANTYHLXGSMNDQTKOQPNQNAV 405
DB 315 SSGRNLSAREPSQKCTEMDCPRE-----TMVSKM-----LDRLHLEEPSGAPVG 358
OY 406 NREERRR-----RVSHDPAQORPEYENFQNTGCKGTIVYSASASHGNAVHQPSGL 455
DB 359 KCPERQADQTSVGRTPARTSSDPA-----GT----- 386
OY 456 TSQPOVLYQNGLYSSHSGFGTRPLDPCGTAGRWVYRPIPSHMPSLHNTIPVETNY--LG 512
DB 387 ---PQI-----PHTLPFRGTTPG-----PVFTEDPGPH-----PQRNGDGRH 421
OY 513 NTFPMPSLSLPTDSEIKTYITINSIGDIGAAYNIHEIGCTSSLLDSTNTNFKEPAAKY 572

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Db      422 CTPWVPMVPMPNPGCPALPVNNCSQEVIGIWN-----SLVAPPRTT--ASSSAKY 470
OY      573 -QAIF 576
         |||
Db       471 DQAOF 475

RESULT 6
RK2_MOUSE
ID RK2_MOUSE STANDARD: PRT; 539 AA.
AC P58801.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 [EC 2.7.1.-].
GN RIKP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21891093; PubMed=11894097;
RA Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G.;
RT "Involvement of receptor-interacting protein 2 in innate and adaptive
   immune responses.";
RL Nature 416:190-194(2002).
CC -1- FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB (by similarity).
CC -1- SUBUNIT: Binds to CFLAR/CFLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2. TRAF1, TRAF2, TRAF5 and
CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- PTM: Autophosphorylated (by similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
-----
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-----
CC EMBL; AF461040; ALX96436.1; .
DR PROSITE; PS50209; CARD. 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM. 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS00108; PROTEIN_KINASE_ST_1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
FW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN_KINASE.
FT DOMAIN 431 523 CARD.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP (BY SIMILARITY).
FT ACT_SITE 146 146 BY SIMILARITY.
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 539 AA; 60400 MW; 42951BF9CA15DFA CRC64;

Query Match * 10.6%; Score 374; DB 1; Length 539;
Best Local Similarity 30.0%; Pred. No. 5,6e-15;
Matches 100; Conservative 67; Mismatches 126; Indels 40; Gaps 10;
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OY 170 NEHNELREVDGTAKNGTLYYAPPEHLNDVNAKPTERS-----DYVSAVVLMAIFA 223
DB 178 SRSYKSAPE-----GGTIYMPPE-----NYPGQKSRASVYKHDIYSVAVIMWEVLS 224
OY 224 NKEPEVNAICBQOLIMCJSGNRPRVDDITECPREI-----ISLMKICWENPAREPT 277
DB 225 RKQPEEVYTNPLQIMYSVQGRPTPSE--ENLPDPIDPHRGIMISLISQGMQNDPERS 282
OY 278 FPGIEKRPFPYLSQLESVEEDVSKLKEYSNEVAVKRMQSLQLD-CVAVSSRSNSA 336
DB 283 FLKCLIELEPVLRPTEDITFLEAVYQLKAKIQQSSSTHLCDRKMDLSLNIPANHPPE 342
OY 337 TEQPELSHSSQGLGMPVEESMFAPSLHPQEE 369
DB 343 ESCGSSLSRMTGSPGP-----SRSLSAPOK 369

RESULT 7
RIRK2_HUMAN STANDARD; PRT; 540 AA.
AC Q4353;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Receptor-interacting serine/threonine protein kinase 2 (BC 2.7.1.-)
DE (RIP-2) (CARD-containing interleukin-1 beta converting enzyme
DE associated kinase) (CARD-containing IL-1 beta ICE-kinase).
DE RIPK2 OR RICK OR RIP2 OR CARDIAK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
[1]
RN RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RX MEDLINE=98241596; PubMed=9575181;
RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
RT "RICK, a novel protein kinase containing a caspase recruitment domain,
RT interacts with CLARP and regulates CD95-mediated apoptosis.";
RL J. Biol. Chem. 273:12296-12300(1998).
[2]
RN RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
RX TISSUE-Endothelial cells;
RX MEDLINE=98307936; PubMed=9642260;
RA McCarthy J.V., Ni J., Dixit V.M.;
RT "Rip2 is a novel NF-kappaB-activating and cell death-inducing
RT kinase.";
RL J. Biol. Chem. 273:16968-16975(1998).
[3]
RN RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.
RX MEDLINE=98381580; PubMed=9705938;
RA Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
RA Mattmann C., Tschopp J.;
RT "Identification of CARDIAK, a RIP-like kinase that associates with
RT caspase-1.";
RL Curr. Biol. 8:885-888(1998).
[4]
RN RP SEQUENCE FROM N.A.
RA Ozeresky P., Holmes A., Brody M.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.
RA Platzner M., Varon R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[6]
RN RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Activates pro-caspase-1 and pro-caspase-8. Potentiates
CC CASP-8-mediated apoptosis. Activates NF-kappaB.
CC - SUBUNIT: Binds to CLARP/CLARP and CASP1 via their CARD domains.
CC Binds to BIRC3/c-IAP1 and BIRC2/c-IAP2, TRAF1, TRAF2, TRAF5 and

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CC TRAF6. May be a component of both the TNFRSF1A and TNFRSF5/CD40
CC receptor complex.
CC - SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC - TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung,
CC peripheral blood leukocytes, spleen, kidney, testis, prostate,
CC pancreas and lymph node.
CC - PTM: Autophosphorylated.
CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC - SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC
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CC or send an email to license@isb-sdb.ch).
CC
DR EMBL, AF027706; AAC34970.1; -
DR EMBL, AF078530; AAC27722.1; -
DR EMBL, AF064824; AAC25668.1; -
DR EMBL, AC004003; AAC24561.1; -
DR EMBL, AF117829; AAD04634.1; -
DR EMBL, BC004553; AAH04553.1; -
DR Genew; HGNC:10020; RIPK2.
DR MIM: 603455; -
DR InterPro: IPR001315; CARD.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Transfaser; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Apoptosis.
FT DOMAIN 18 294 PROTEIN KINASE.
FT DOMAIN 432 524 CARD.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP.
FT ACT_SITE 146 146
FT MUTAGEN 47 47 K->A: ABOLISHES KINASE ACTIVITY.
FT MUTAGEN 146 146 K->M: REDUCES PAS-MEDIATED APOPTOSIS.
FT MUTAGEN 146 146 D->N: ABOLISHES KINASE ACTIVITY.
SQ SEQUENCE 540 AA: 61194 MW: 575A692239505792 CRC64;

Query Match 10.5%; Score 371; DB 1; Length 540;
Best Local Similarity 28.8%; Pred. No. 8.4e-15;
Matches 112; Conservative 68; Mismatches 145; Indels 64; Gaps 12;

OY 23 LDSGFGKVSICFH--RTQGLIMTKTYKGPNCIEHNEALLERAKMNRRLRHSRYVKL 79
DB 24 LSRGASGVSSARADRWQ-VAVKHLIHHPLLDSEKRDVLRAREILHKRARSYILPIL 82
OY 80 GVITIEGYSLVMEYMEGNLMHLKAMKSP--LSYKGIILIEITIEGKCYLNG--KGV 134
DB 83 GICNEPFLGIVTEYMPGSLNELIHRTEXPDVAMPPLRFLIHEIALGVVYLNHPPL 142
OY 135 IAKDLKPNILVNDNFHFKIADLGASFKMSKLNNEHNEHLREVDGTAKNGTLYYMA 194
DB 143 LHHDLKTONIILNDEFHFKINDPGLSKRMMSLSQSSKSAPE-----GGTIYMP 194
OY 195 PEHLNDVNAKPTERS-----DYVSAVVLMAIFANKEPYENALCEQOLIMCJSGNRPD 248
DB 195 PE-----NYPGQKSRASIKRDIYSVAVITWEVLSRQPFEDVNNPIQIMYSVQGRPV 249
OY 249 VDDITEYCPREI-----ISLMKICWENPAREPTFQIEKRPFPYLSQLESVEEDVK 302
DB 250 INE--ESLPDIPHRARMTSLIESGMQNDPERSFLKCLTELEPVLRTFEEITFLEAVI 307

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[illegible]

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DB      1168 KSGKGLPVWMSPESLKD--GVFTYYSVWMSGVVLWELATLAEQYOGLSNEQVLRFY 1225
      241 IKSG--NRDVEDITFCPEREIISLMKLCMEANPEARPTFGCELEFRFPYISQLESSE 298
      1226 MEGGLDLPD-----NCPDMLFELMRKWCQYNPKRPSFLET-----ISIKEEME 1271
OY      299 EDVKSLKREYSNENAV-----VKRQSLQDLCVAVPSSRSNATQPGSLHSSQGL 349
      1272 PGFRVSEFYSEENKLPPEPELDLPENNESVPLD-----PSASSSLPLP-DRHSGH-- 1323
DB      350 GNGVVEESWPAFSLHEHQEENEPS-----LQSKLQDEANV-HLYGSRMDQTKQOPRON 402
      1324 -----KAENCGPGCVLVRASFDEROPAHNNGRKNRRLPLPOSS 1365

RESULT 10
MATK_RAT
ID      MATK_RAT      STANDARD:      PRT:      467 AA.
AC      P41243:
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      01-FEB-1995 (Rel. 31, Last annotation update)
DE      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)
GN      (Tyrosine-protein kinase CTK) (Protein kinase BAKT).
OC      MATK OR CTK OR BAKT.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RA      MEDLINE=95106341; PubMed=7807586;
RA      Kuo S.S., Moran P., Gripp J., Armanini M., Phillips H.S., Goddard A.,
RA      Caras I.W.;
RT      Identification and characterization of Bakt, a predominantly brain-
RT      specific non-receptor protein tyrosine kinase related to Csk.;
RT      J. Neurosci. Res. 38:705-715(1994)
RL      J. Neurosci. Res. 38:705-715(1994)
CC      -1- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION
CC      OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF
CC      SRC-FAMILY MEMBERS IN BRAIN.
CC      -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC      tyrosine phosphate.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- TISSUE SPECIFICITY: ENRICHED IN LYMPHOID TISSUES.
CC      -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
CC      SUBFAMILY.
CC      -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC      -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: L34542; AAA64524.1; -
DR      HSSP: P11362; 1FGK.
DR      InterPro: IPR000719; Euk_pkinase.
DR      InterPro: IPR000980; SH2.
DR      InterPro: IPR001452; SH3.
DR      InterPro: IPR001245; Tyr_kinase.
DR      Pfam: PF00017; SH2; 1.
DR      Pfam: PF00018; SH3; 1.
DR      Pfam: PF00069; pkinase; 1.
DR      PRINTS: PR000401; SH2DOMAIN.
DR      ProDom: PD000001; Euk_pkinase; 1.
DR      ProDom: PD000093; SH2; 1.
DR      SMART: SM00252; SH2; 1.
DR      SMART: SM00326; SH3; 1.

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DR      SMART: SM00219; TYRKc; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE: PS50001; SH2; 1.
DR      PROSITE: PS50002; SH3; 1.
KW      transferase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
KW      SH3 domain; Phosphorylation.
FT      DOMAIN      22      69      SH3.
FT      DOMAIN      81      170      SH2.
FT      DOMAIN      194      443      PROTEIN KINASE.
FT      NE_BIND      200      208      ATP (BY SIMILARITY).
FT      BINDING      221      221      ATP (BY SIMILARITY).
FT      ACT_SITE      311      311      BY SIMILARITY.
SQ      SEQUENCE      467 AA; 51896 MW; 283FF9348B5FA8F CRC64;

Query Match      9.7%; Score 343; DB 1; Length 467;
Best Local Similarity 33.2%; Pred. No. 3; Le-13;
Matches      89; Conservative 47; Mismatches 100; Indels 32; Gaps 9;

OY      21 AELDSGFGKVSICFHRQGLMT-MKTVYKGPNCIEHNEALLBEAKMNRRLRSRYKLL 79
      198 AQTGESEFGAV-----LQGEYLQGVAVANIKCDVTAQAFDETAVMKLOHRNLVRL 251
DB      80 GVITEERKYSLVMEYERKGLMHVLAEMSTPLSVKG--RIILEITGCMCYLHGKGVYHK 137
      252 GVILHHGLY-TVNEHYSKGLVNFPLTRGRALVSTSOLOFALHVAEGMETLSKLVHR 310
OY      138 DLKPENILVNDNEFHIAIADGLASFPMKSKLNNEHNEHLEVDGTAKKNGTLYVNAPEH 197
      311 DLARNILVSEDLVAVVSDFGAKAEIKGLDSSRL-----PVKMTAPEA 355
DB      198 LNDVNAKPTKESVYSFAVVLMAIFA-NKRPYENALICEQOLMCISGNRPVDDITTEYC 256
      356 LK--NGRFSSKQVSWMSGVGLMEVFSYGRAPYKR-MSLKREVSBAVEKGYRMEPPD---SC 409
OY      257 PRETISLMKLCWEANPEARPTFGIEEK 284
      410 PGVHTLMGSCWEAFPSRRPFKRYEK 437
DB

RESULT 11
IGIR_BOVIN
ID      IGIR_BOVIN      STANDARD:      PRT:      640 AA.
AC      Q05688;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Insulin-like growth factor I receptor precursor (EC 2.7.1.112)
DE      (Fragment).
GN      IGfIR.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovine; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RX      MEDLINE=92119330; PubMed=1662995;
RA      Sneyers M., Kettmann R., Massart S., Renaville R., Burry A.,
RA      Portetelle D.;
RT      Cloning and characterization of a cDNA encoding the beta-subunit of
RT      the bovine insulin-like growth factor-1 receptor.;
RL      DNA Seq. 1:405-406(1991).
CC      -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
CC      WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
CC      TYROSINE-PROTEIN KINASE ACTIVITY.
CC      -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC      tyrosine phosphate.
CC      -1- SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide
CC      bonds. The alpha chains contribute to the formation of the ligand-
CC      binding domain, while the beta chain carries the kinase domain.

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CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
DR EMBL: X54980; CA38724.1; -.
DR HSSP: P06213; IIRK.
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR002011; RTKinaseII.
DR InterPro: IPR001245; Tyr-kinase.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00069; kinase; 1.
DR ProDom: PD000001; Euk-kinase; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
DR Transfaser: Tyrosine-protein kinase; Receptor; Transmembrane;
KW Glycoprotein; ATP-binding; Phosphorylation; Repeat.
FT CHAIN 1 13
FT <1 13
FT CHAIN 14 640
FT 14 640
FT TRANSMEM 14 208
FT DOMAIN 209 232
FT DOMAIN 233 640
FT DOMAIN <1 101
FT DOMAIN 102 201
FT DOMAIN 272 547
FT NP_BIND 278 286
FT BINDING 306 306
FT ACT_SITE 408 408
FT MOD_RES 438 438
FT CARBOHYD 20 20
FT CARBOHYD 29 29
FT CARBOHYD 37 37
FT SEQUENCE 640 AA: 72511 MW; 1E645258BDC6FEF29 CRC64;
Query Match 9.7%; Score 342.5; DB 1; Length 640;
Best Local Similarity 27.9%; Pred. No. 5e-13;
Matches 116; Conservative 67; Mismatches 148; Indels 85; Gaps 18;

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OY 20 SAELDSGGFGKY-----SLCFHRTQGLIMKTYKCGNCTJHNFALLEAKMNRRLHS 73
DB 275 SRELGGSGFGYEVGAVGVKDEPETHVAIKTVNEAASMERIE-FLNEASVMEFNC 333
OY 74 RVKVLGVIEEGKSYLVEYMEKGNL--MHVLKAES-----TPLSVKGRIIL-ELI 123
DB 334 HVRVLGVVSGOGLPTVLMELMTKGLSLASLSEPEENNEVLAAPSLSKWIMQAGEIA 393
OY 124 EGMCYLHGKGVYIHKDKLEPILVNDPEFIKTIADIGLASFKMKSKMLNNEHNEHLEPVDGTA 183
DB 394 DGMAVLYNANKFVHDLARNCVMAEDFTVKTIGDGMT-----RDITYETDYR 440
OY 184 KKNKGTLL--TYMAEHLNDVNAKPTKESDVSEFVNLMAIFA-NKEPYENAIICQOLIMC 240
DB 441 KGGGLPVRKMSSESLKD--GVFTTSDVWSFGVVLMEIATLAEQPYQGLSNDOVLRFV 498
OY 241 IKSG--NRPDVDDITECPREIISLMKLCWANEAPRTFGIEKRPPLTSLQLESSEV 298
DB 499 MEGSLDKPD-----NCPDMLFELMRKWCWOYNPKMRPSFLEI-----ISSVKDEME 544

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RESULT 12

ID	IGIR_RAT	STANDARD	PRT	1370 AA.
AC	P24062			
DT	01-MAR-1992 (Rel. 21, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Insulin-like growth factor I receptor precursor (EC 2.7.1.112).			
GN	IGF1R			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=95277910; PubMed=7758167;			
RA	Du J., Delafontaine P.;			
RT	"Inhibition of vascular smooth muscle cell growth through antisense			
RT	transcription of a rat insulin-like growth factor I receptor cDNA.";			
RL	Circ. Res. 76:963-972(1995).			
RN	[2]			
RP	SEQUENCE OF 1-364 FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RX	MEDLINE=90017496; PubMed=2477843;			
RA	Werner H., Woloschak M., Adamo M., Shen-Orr Z., Roberts C.T. Jr.,			
RT	Leroith D.;			
RT	"Developmental regulation of the rat insulin-like growth factor I			
RT	receptor gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 86:7451-7455(1989).			
RN	[3]			
RP	SEQUENCE OF 913-1017 FROM N.A.			
RX	MEDLINE=92412145; PubMed=1530648;			
RA	Kurachi H., Jobo K., Ohta M., Kawasaki T., Itoh N.;			
RT	"A new member of the insulin receptor family, insulin			
RT	receptor-related receptor, is expressed preferentially in the			
RT	kidney.";			
RL	Biochem. Biophys. Res. Commun. 187:934-939(1992).			
CC	-1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)			
CC	WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A			
CC	TYROSINE-PROTEIN KINASE ACTIVITY.			
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC	tyrosine phosphate.			
CC	-1- SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide			
CC	bonds. The alpha chains contribute to the formation of the ligand-			
CC	binding domain, while the beta chain carries the kinase domain.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN			
CC	RECEPTOR SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC				
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: L29232; AAA41392.1; -.			

DR	InterPro:	IPR000494;	EGRF_Ldomain.
DR	InterPro:	IPR000719;	Euk_Pkinase.
DR	InterPro:	IPR003961;	FN_III.
DR	InterPro:	IPR002174;	Furin-like.
DR	InterPro:	IPR002011;	RtkinasetI.
DR	InterPro:	IPR001245;	Tyr_pkinase.
DR	Pfam:	PF00041;	fn3; 2.
DR	Pfam:	PF00069;	pkinaase; 1.
DR	Pfam:	PF00757;	Furin-like; 1.
DR	Pfam:	PF01030;	Recep_Ldomain; 2.
DR	PRINTS:	PR00109;	TYRKINASE.
DR	ProDom:	PD000001;	Euk_Pkinase; 1.
DR	SMART:	SM00260;	FN3; 3.
DR	SMART:	SM00261;	FU3; 1.
DR	SMART:	SM00219;	Tyrc; 1.
DR	PROSITE:	PS00107;	PROTEIN_KINASE_ATP; 1.
DR	PROSITE:	PS00109;	PROTEIN_KINASE_TYR; 1.
DR	PROSITE:	PS00239;	RECEPTOR_TYR_KIN_II; 1.
DR	PROSITE:	PS50011;	PROTEIN_KINASE_DOM; 1.
KW	Transfaser:	Tyrosine-protein kinase; Receptor;	Transmembrane;
KW	Glycoprotein:	ATP-binding; Phosphorylation; Repeat; Signal.	POTENTIAL.
FT	SIGNAL	1	30
FT	CHAIN	31	741
FT	CHAIN	742	1370
FT	CHAIN	742	1370
FT	DOMAIN	742	936
FT	TRANSMEM	937	960
FT	DOMAIN	961	1370
FT	DOMAIN	608	829
FT	DOMAIN	830	929
FT	DOMAIN	1000	1275
FT	NP_BIND	1006	1014
FT	BINDING	1034	1034
FT	ACT_SITE	1136	1136
FT	DISULFD	215	224
FT	DISULFD	219	230
FT	DISULFD	231	239
FT	DISULFD	235	248
FT	DISULFD	251	260
FT	DISULFD	264	276
FT	DISULFD	282	303
FT	DISULFD	307	321
FT	DISULFD	324	328
FT	CARBOHYD	51	51
FT	CARBOHYD	102	102
FT	CARBOHYD	135	135
FT	CARBOHYD	245	245
FT	CARBOHYD	314	314
FT	CARBOHYD	418	418
FT	CARBOHYD	439	439
FT	CARBOHYD	535	535
FT	CARBOHYD	608	608
FT	CARBOHYD	623	623
FT	CARBOHYD	641	641
FT	CARBOHYD	748	748
FT	CARBOHYD	757	757
FT	CARBOHYD	765	765
FT	CARBOHYD	901	901
FT	CARBOHYD	914	914
FT	MOD_RES	1166	1166
FT	CONFLICT	985	986
SO	SEQUENCE	1370 AA;	155395 MM; 155395 CRC64;

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Query Match Similarity: 9.6%; Score 339.5; DB 1; Length 1370;
Best Local Similarity: 27.6%; Pred. No. 2,1e-12;
Matches 116; Conservative 64; Mismatches 144; Indels 97; Gaps 19;
OY 22 ELDSGGRKY-----SLCFHRTQGLIMTKYVYKCPNCLTENHALLLEAKMMNRLRHSRY 75
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1005 ELGGGSFQWYEGVAKGVYKDEPEFRVAKITVYNAASRRERLE-FLNLSAVYKFEFNCHV 1063K
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 76 VKLLGVIIIEEGKYSLSWETMERKGNIMHLKAKEMSTPLSVKGRIL-----EI 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db	1064	VRLLGVSSQCPPTLVIMELMTRGDLKSYLR---	SLREPEVENNLVLPISLSKMTOMAGET	1120
Qy	123	TEGMCVLHGKGVIIHKDKPENITLVNDNFHIIKADI	GLASFEMSKLNNEEHNELREVGD	182
Dd	1121	ADGMAVYLNANKFVIRHDLAARNCMAVEDPTVAK	IGDFGMT-----	RDLEYDY 1167
Qy	183	AKKNGGTL--YMAPEHLNDVNAKPTKSDVYSFAVYL	MAIFA-NKEPYENALCEQOLIM	239
Dd	1168	RKGGKGLLPVAKMSPESLKD--GVETTHSDWSG	VYLMETATLAEOPYGLSMEQVLR	1225
Qy	240	CIRSG--NRPDVDITEYCPRELLISMLKICMEAP	PEARPRF-----	PIEEKFRP----- 287
Dd	1226	VMEGGLDKDP-----NCPDMLLELMKMCQY	NPKRPSFLLETIGSKIDMEFSFOEVS	1279
Qy	288	FYLSLEESVEEDVYSLKKEYSNENAVAKRMSQ	LDLCVAVPSRSNSATEQPSLHSQ	347
Dd	1280	FYISEENKPPPELELMELIEPPN-----	MESVPLD-----	PSASSASL----- 1319
Qy	348	GLGMPVEESMFADSLHP--QEENEPS--	LSQSLQDEANY-HLYSRMDRQTKQOPRQ	401
Dd	1320	-----PIPE-----	RHSGHKAENGCGVILRASFPDRQPYAHMNGRAN	RALPLPOS 1367
Qy	402	N 402		
Dd	1368	S 1368		

RESULT 13

ID	MATK_MOUSE	STANDARD:	PRT:	505 AA.
AC	P41242:			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)			
DE	(Tyrosine-protein kinase Ctk) (Protein kinase NTK).			
GN	Mus musculus (Mouse).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090.			
RN	[1]			
RP	SEQUENCE OF 41-505 FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=94195789; PubMed=7511815;			
RA	Klages S., Adam D., Class K., Fargnoli J., Boien J.B.,			
RA	Penhallow R.C.;			
RT	"Csk: a protein-tyrosine kinase related to Csk that defines an enzyme			
RT	family.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:2597-2601(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BAIB/C; TISSUE=Thymus;			
RA	MEDLINE=94255451; PubMed=8197166;			
RA	Chow L.M.L., Jarvis C.D., Hu Q., Nye S.H., Gervais F.G.,			
RA	Veillelette A., Matis L.A.;			
RT	"Ntk: a Csk-related protein-tyrosine kinase expressed in brain and T			
RT	lymphocytes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 91:4975-4979(1994).			
RN	[3]			
RP	SEQUENCE OF 41-505 FROM N.A.			
RC	STRAIN=DDY/STD;			
RX	MEDLINE=95206787; PubMed=7898936;			
RA	Kaneko Y., Nonoguchi K., Fukuyama H., Takano S., Higashitsuji H.,			
RA	Nishiyama H., Takenawa J., Nakayama H., Fujita J.;			
RT	"Presence of alternative 5' untranslated sequences and identification			
RT	of cells expressing ctk transcripts in the brain and testis.";			
CC	Oncogene 10:945-952(1995).			
CC	-i- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION			
CC	OF HEMATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF			
CC	SRC-FAMILY MEMBERS IN BRAIN BY SPECIFICALLY PHOSPHORYLATING THEIR			
CC	C-TERMINAL REGULATORY TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE			

RA Kanieko Y, Nonoguchi K., Fukuyama H., Takano S, Higashitsunji H.,
 RA Nishiyama H., Tatenaka J., Nakayama H., Fujita J., and identification
 RT "presence of alternative 5' untranslated sequences and identification
 of cells expressing cti transcripts in the brain and testis.";
 RL Oncogene 10:945-952(1995).
 CC -I- FUNCTION: COULD PLAY A SIGNIFICANT ROLE IN THE SIGNAL TRANSDUCTION
 CC OF HEPATOPOIETIC CELLS. MAY REGULATE TYROSINE KINASE ACTIVITY OF
 CC SRC-FAMILY MEMBERS IN BRAIN BY SPECIFICALLY PHOSPHORYLATING THEIR
 CC C-TERMINAL REGULATORY TYROSINE RESIDUE WHICH ACTS AS A NEGATIVE

CC REGULATORY SITE. IT MAY PLAY AN INHIBITORY ROLE IN THE CONTROL OF
CC T-CELL PROLIFERATION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (probable).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing. Isoform 2 is the less abundant
CC form.
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, AND TO A LESSER EXTENT
CC IN THE SPLEEN, THE THYMUS AND THE LIVER. ALSO FOUND IN THE T-CELL
CC LINEAGE.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. CSK
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL: U05210; AAA18829.1; -
DR EMBL: L27738; AAB59677.1; -
DR EMBL: D45243; BAA08199.1; -
DR HSSP: P11362; IFGK.
DR MGD: MGI:99259; Mark.
DR InterPro: IPR000719; Euk_Dkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRODOM: PD000001; Euk_Pkinase; 1.
DR PRODOM: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TyrcK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW Transferrase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
KW SH3 domain; Phosphorylation; Alternative splicing.
FT DOMAIN 61 108
FT DOMAIN 120 209
FT DOMAIN 233 481
FT NP_BIND 239 247
FT BINDING 260 260
FT ACT_SITE 350 350
FT VARSPIC 43 43
FT CONFLICT 105 106
SQ SEQUENCE 505 AA; 56056 MW; 0A1661C1FBFD6A53 CRC64;
Query Match 9.5%; Score 338.5; DB: 1; Length 505;
Best Local Similarity 33.6%; Pred. No. 6.3e-13;
Matches 90; Conservative 46; Mismatches 99; Indels 33; Gaps 10;
QY 21 AELDGGFGKVSICFHTRTGIMI-MKTVYKGPNCIEHNEALIEBKMMNRLRHSRVKLL 79
DB 237 AQGCEGFAY-----LQGEYLGQKVAVNINIKCDVTAQAFLDSTAVMTKIQHNINLVRL 290
QY 80 GVIEESKISLVMEYMEKGMILHVKAKEMSTPLSVKG--RIIEIEGKCYLHGKGVYIK 137
DB 291 GVILIHGLY-IVMEHVSNGMLVNEFLRTGRALVSTQLQFALHVAEGMEYIESKRLVHR 349
QY 138 DLAPENLVNDHFIKADIAGLASFKMKSKLNNEHNELEFVNDSTAKNGSTLYAPPEH 197

DB 350 DLAAKNILVSEDLVAKVSPFLAK-----AEKGLDSSRL-----PVKWTAPEA 393
QY 198 LNDVNAKPFKESDVYSFAVLMAIJA-NKEPYENAIICQQLIMKISGNRPVDVDFEYC 256
DB 394 LK--NGRFSSKSDWSFEVLMEVFSIGRAPPK-MSIKEVSEAVEKGRMEPPD--GC 447
QY 257 PREIISLMKLCWEANPEARPTPEIEEK 284
DB 448 PGSVHTLMGSCWEAEAPARRPFRKIVEK 475
RESULT 14
IGIR_MOUSE STANDARD: PRT: 1373 AA.
AC 060751; 062123; 070438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update).
DT 15-JUN-2002 (Rel. 41, Last annotation update).
DE Insulin-like growth factor I receptor precursor (EC 2.7.1.112).
GN IGPIR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT-Taxid-10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Navarro M., Garandel V., Barenton B., Bernardi H.;
RT "Cloning of cDNA for the mouse insulin-like growth factor I
RT receptor."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-329 FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney;
RA Jun W., Liu Z., Alvares K., Kumar A., Wallner E.I., Kanwar Y.S.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1134-1203 FROM N.A.
RX MEDLINE=90152381; PubMed=2482828;
RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
RT "The application of the polymerase chain reaction to cloning members
RT of the protein tyrosine kinase family."
RL Gene 85:67-74(1989).
CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
CC WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
CC TYROSINE-PROTEIN KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide
CC bonds. The alpha chains contribute to the formation of the ligand-
CC binding domain, while the beta chain carries the kinase domain.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC RECEPTOR SUBFAMILY
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: AF056187; AAC12782.1; -
DR EMBL: U00182; AAC52123.1; -
DR EMBL: M33422; AAA40013.1; -
DR HSSP: P06213; IIRK.
DR MGD: MGI:96433; Igflr.
DR InterPro: IPR000494; EGFR_L_domain.
DR InterPro: IPR000719; Euk_Dkinase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002011; RTK_inseII.

DR InterPro: IPR001245; Tyr-kinase.
 DR Pfam: PF00041; fn3. 2.
 DR Pfam: PF00069; kinase. 1.
 DR Pfam: PF00757; Furin-like. 1.
 DR Pfam: PF01030; Recep_L-domain. 2.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk-kinase. 1.
 DR SMART: SM00060; FN3. 3.
 DR SMART: SM00261; FU. 1.
 DR SMART: SM00219; TYKC. 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR. 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
 DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II. 1.
 DR Transferrase: Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
 KM Glycoprotein; ATP-binding; Phosphorylation; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 741
 FT CHAIN 742 1373
 FT CHAIN 742 1373
 FT DOMAIN 742 936
 FT TRANSFER 937 960
 FT DOMAIN 961 1373
 FT DOMAIN 608 829
 FT DOMAIN 830 929
 FT DOMAIN 1000 1276
 FT NE_BIND 1006 1014
 FT BINDING 1034 1034
 FT ACT_SITE 1137 1137
 FT DISULFID 215 224
 FT DISULFID 219 230
 FT DISULFID 231 239
 FT DISULFID 235 248
 FT DISULFID 251 260
 FT DISULFID 264 276
 FT DISULFID 282 303
 FT DISULFID 307 321
 FT DISULFID 324 328
 FT CARBOHYD 51 51
 FT CARBOHYD 102 102
 FT CARBOHYD 135 135
 FT CARBOHYD 245 245
 FT CARBOHYD 314 314
 FT CARBOHYD 418 418
 FT CARBOHYD 439 439
 FT CARBOHYD 453 453
 FT CARBOHYD 535 535
 FT CARBOHYD 608 608
 FT CARBOHYD 623 623
 FT CARBOHYD 641 641
 FT CARBOHYD 748 748
 FT CARBOHYD 757 757
 FT CARBOHYD 765 765
 FT CARBOHYD 901 901
 FT CARBOHYD 914 914
 FT MOD_RES 1167 1167
 FT CONFLICT 58 59
 FT CONFLICT 260 260
 FT CONFLICT 301 301
 FT CONFLICT 306 306
 FT CONFLICT 324 324
 FT CONFLICT 1134 1134
 FT CONFLICT 1145 1145
 FT CONFLICT 1202 1202
 SQ SEQUENCE 1373 AA; 155787 MW; 5EB3B72EF101B379 CRC64;

Query Match 9.58; Score 338; DB 1; Length 1373;
 Best Local Similarity 27.08; Pred. NO. 2.6e-12;

Matches 113; Conservative 65; Mismatches 152; Indels 88; Gaps 16;

QY 22 ELDSGGGFGKY-----SLCFHRTQGLIMKTVYKGPICIEHNEALLBEAKMKNLRSRV 75
 DB 1005 ELDSGGSGMYEGYAKGVAVDEPETRAVIAITVNAASMRERIE-FLNEASVMKEFNCHV 1063

QY 76 VKLLGVITIEGSKYSLVMEYMEKGNLMHVKA-----EMSTPLSYKGRITL 120
 DB 1064 VRLGLVVSQGOPTLVIMELTRGDKSLVLSLRPEVDONNLVLIPSLSKMIONAG---- 1119
 QY 121 EIEEGMCYLHGKGVYHNDLKPENILVNDPIFIKADIGLASFMMKSLNNEHNEHLEVD 180
 DB 1120 EIDAGMAYLVNAKRVHNDLAARNCMAVEDFVKIGDGMT-----RDITETD 1166
 QY 181 GTAKKNGCTL--YYAPEHLNDVNAKPTKSDVYSFAVVLMAIFA-NKEPYENALICEQL 237
 DB 1167 YRRRGCGGLLPVRMWSPELKD--GVFTTSDVMSFGVLMETIALEQPYOGLSNROYL 1224
 QY 238 IMCKISG--NRPDVDDITFCPRFIIISLMKLCWANEARTF----PGIEKRP----- 287
 DB 1225 REVVEGGLLKPDP-----NCPDMLFELMRWCWYNRMRPSFLEIGISKDEHPSFQE 1278
 QY 288 --FYLSQLSEESVEDVSLKKEYSNEAAYVARMOSLODCVAVPSSRSNSATQPGSLHS 345
 DB 1279 VSFYISEENKRPPEPELEMELEMPEN-----MESVFLDPSA--SSASLPLEKHSCHKA 1331
 QY 346 SGLGKMPVEESWEFAPSLHEPQEEHNPSSLOSKLQDEANY-HLYGSRMDRQTKQOPRON 402
 DB 1332 ENCGPGVLT-----VLRASFDERQPYAHMNGCRANERLALPPOSS 1371

RESULT 15
 MATR_HUMAN STANDARD; PRT; 507 AA.
 ID MATR_HUMAN
 AC P42679;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112)
 DE (Tyrosine-protein kinase CTK) (Protein kinase HYL) (Hematopoietic
 DE consensus tyrosine-lacking kinase).
 GN MARK OR CTK OR HYL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94181267; PubMed=8134117;
 RA Sakano S., Iwama A., Inazawa J., Ariyama T., Ohno M., Suda T.;
 RT "Molecular cloning of a novel non-receptor tyrosine kinase, HYL
 RT (hematopoietic consensus tyrosine-lacking kinase).";
 RL Oncogene 9:1155-1161(1994).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Megakaryocytes;
 RX MEDLINE=94117408; PubMed=8288563;
 RA Bennett B.D., Cowley S., Jiang S., London R., Deng B., Grabarek J.,
 RA Groopman J.E., Goeddel D.V., Avraham H.;
 RT "Identification and characterization of a novel tyrosine kinase from
 RT megakaryocytes.";
 RL J. Biol. Chem. 269:1068-1074(1994).
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95130565; PubMed=7530249;
 RA Avraham S., Jiang S., Ota S., Fu Y., Deng B., Dowler L.L.,
 RA White R.A., Avraham H.;
 RT "Structural and functional studies of the intracellular tyrosine
 RT kinase MARK gene and its translated product.";
 RL J. Biol. Chem. 270:1833-1842(1995).
 RP SEQUENCE FROM N.A.
 RA Lamerlin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,

```

DR PROSITE PS50001; SH2; 1.
DR PROSITE PS50002; SH3; 1.
KW Transferase: Tyrosine-protein kinase; ATP-binding; SH2 domain;
KW SH3 domain; Phosphorylation.
FT DOMAIN 58 110 SH3.
FT DOMAIN 122 211 SH2.
FT DOMAIN 235 482 PROTEIN KINASE.
FT NP_BIND 241 249 APP (BY SIMILARITY).
FT BINDING 262 262 APP (BY SIMILARITY).
FT ACT_SITE 352 352 BY SIMILARITY.
FT CONFLICT 107 108 ER -> DG (IN REF. 1).
FT CONFLICT 400 400 MISSING (IN REF. 1).
FT CONFLICT 466 507 ARPPRKLAETLARELSAGAPASVSGODAGSTSPRSOE
P -> PAPHGSANWPSRMSGSYAVOVQPPSPQGRTPYHLA
PKPGALTPPGSGWPPORTERVESAAWGH (IN REF. 1).
SO SEQUENCE 507 AA; 56469 MW; 85721C6E024575EF CRC64;

Query Match 9.5%; Score 337.5; DB 1; Length 507;
Best Local Similarity 32.6%; Pred. No. 7.2e-13;
Matches 90; Conservative 47; Mismatches 90; Indels 49; Gaps 111

QY 21 AELDSGFGKVSICFHRTOGLMI-KTYVYKGPNCIEHNEALLERKMMNRLRHSRVYKL 79
Db AQTGESEFGAV-----LQGEYLQGVAVAKNKICDVTAAQAFIDETAVMTKQHEHNLVRL 292
QY 80 GVILIEGKYSLVWEYMEKGNLMHVLKAEKSTPLSVKGRLL-----LEIEGMCYL 129
Db GVILHGGIV-IYWEHVSKGKNLVNFRL-----TRGALVNTAQQLQSLHVAEGMEYL 343
QY 130 HGKGVYHKDLKRPENIIVDNDPIIKTADLGLASFEKMWSKLNEEHNEELREYDGTAKKNGT 189
Db ESKRLVHRDLAARNIIVSDDLVAKVSDFGLAKE-----AERKGLDSRL---P 387
QY 190 LYYMAPEHLDVNAKPTERKSDVYSFAVYVLMATFA-NKEPYENATICEQQLIMCKKSGMRPD 248
Db VKMTADEALK--HGKFTSKSDVMSGCVLLMEYFSTIGRAPYFK-WSLKEVSEAVEKGYRME 444
QY 249 VDDITEYCPREIISLMKLCMEANPEARPTFGIIEK 284
Db P---PEGCGPVPYHLMKSCWMEAPARRPFRKLEAK 477

Search completed: June 21, 2003, 16:13:13
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: June 21, 2003, 16:05:19 ; Search time 87 Seconds
(Without alignments)
1589.168 Million cell updates/sec

Title: US-09-981-397A-16
Perfect score: 3545
Sequence: 1 MOPDKSLNVIKMKSDPLES.....ALHOCGRIDLSSLIYVSON 671

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp._archaea:*
2: sp._bacteria:*
3: sp._fungi:*
4: sp._human:*
5: sp._invertebrate:*
6: sp._mammal:*
7: sp._mhc:*
8: sp._organelle:*
9: sp._phage:*
10: sp._plant:*
11: sp._rodent:*
12: sp._virus:*
13: sp._vertebrate:*
14: sp._unclassified:*
15: sp._virus:*
16: sp._bacteriaph:*
17: sp._archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	410.5	11.6	786	11 09ERK0	09erko mus musculi
2	387	10.9	784	4 096711	096711 homo sapien
3	384	10.8	784	4 09H4D1	09h4d1 homo sapien
4	384	10.8	784	4 096KH0	096kh0 homo sapien
5	361.5	10.2	1412	13 080W84	080w84 paraliichthy
6	360.5	10.2	669	13 091AA2	091aa2 paraliichthy
7	348	9.8	609	13 091776	091776 carassius a
8	347.5	9.8	1671	5 09NIV5	09n1776 xenopus lae
9	346.5	9.8	1418	13 080W83	080w83 biophthalari
10	345.5	9.7	515	13 080UY9	08uy9 biachydanio
11	340.5	9.6	855	5 001700	001700 caenorhabdi
12	339	9.6	488	13 013064	013064 xenopus lae
13	339	9.6	1358	13 073798	073798 xenopus lae
14	338.5	9.5	465	11 09D6H7	09d6h7 mus musculi
15	338.5	9.5	465	11 070223	070223 mus musculi
16	338.5	9.5	511	11 064103	064103 mus sp. vnk

17	338.5	9.5	763	10 09C903	09c903 arabidopsis
18	338.5	9.5	1245	13 09YGH8	09ygh8 scophthalmu
19	338	9.5	1371	11 090YWA	090ywa rattus sp.
20	337.5	9.5	523	4 09N5R8	09n5r8 homo sapien
21	337.5	9.5	777	10 09C833	09c833 arabidopsis
22	337	9.5	989	13 09PWN6	09pwn6 gallus gall
23	336.5	9.5	1171	10 09STG4	09stg4 arabidopsis
24	335	9.4	525	10 08W022	08w022 arabidopsis
25	335	9.4	829	10 024027	024027 lycopersico
26	334.5	9.4	1094	5 023915	023915 dictyostell
27	334	9.4	765	10 093100	093100 arabidopsis
28	334	9.4	1127	5 0908P5	0908p5 diadema set
29	331	9.3	525	10 09F1L6	09f1l6 arabidopsi
30	331	9.3	806	10 09ZSD8	09zsd8 lycopersico
31	331	9.3	829	10 09ZSD9	09zsd9 lycopersico
32	330.5	9.3	527	5 09B125	09b125 dictyostell
33	330.5	9.3	1418	13 093457	093457 scophthalmu
34	329.5	9.3	475	10 09STG5	09stg5 arabidopsis
35	329.5	9.3	2144	5 09VD94	09vd94 drosophila
36	329	9.3	502	13 09DDK6	09ddk6 salmo salar
37	329	9.3	1257	10 064768	064768 arabidopsis
38	329	9.3	1362	13 09PVZ4	09pvz4 xenopus lae
39	329	9.3	1368	13 080W85	080w85 paraliichthy
40	328.5	9.3	405	10 091VQ9	091vq9 arabidopsis
41	328.5	9.3	450	11 08VCW1	08vcw1 mus musculi
42	328.5	9.3	480	10 09FPV7	09fpv7 faqus sylva
43	328.5	9.3	773	10 09C902	09c902 arabidopsis
44	328.5	9.3	1369	13 080W86	080w86 paraliichthy
45	328	9.3	465	4 016176	016176 homo sapien

ALIGNMENTS

RESULT 1
ID 09ERK0 PRELIMINARY; PRT; 786 AA.
AC 09ERK0:
DT 01-MAR-2001 (TREMUREL 16, Created)
DT 01-MAR-2002 (TREMUREL 20, Last sequence update)
DT 01-JUN-2002 (TREMUREL 21, Last annotation update)
DE PKC-regulated kinase PKK.
GN ANKRD3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=21293027; Pubmed=11278382;
RA Chen L., Haidar K., Ponda M., Cariappa A., Rowitch D., Pillai S.;
RT "Protein kinase C-associated kinase (PKK), a novel membrane-associated, ankyrin repeat-containing protein kinase."
RL J. Biol. Chem. 276:21737-21744(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Chen L., Haidar K., Cariappa A., Pillai S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF302127; AGC30871.2; -
DR HSSP: P25963; I1KN.
DR MGD; MGI:1919638; Ankrd3.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF000023; ank. 10.
DR Pfam: PF000069; pkinase. 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRODOM; PD0000001; Euk_pkinase; 1.
DR SMART; SM00248; ANK. 10.
DR SMART; SM00220; S_TKc; 1.

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DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS50088; ANK_REPEAT; 9.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR KINASE.
KW SEQUENCE 786 AA; 86612 MW; 66CE2C25EE96A40C CRC64;

Query Match
Best Local Similarity 31.18; Score 410.5; DB 11; Length 786;
Matches 127; Conservative 73; Mismatches 164; Indels 45; Gaps 16;

QY 14 SSDFLSEALDGGFGKVSCLFHRTQGLMKT---YKGPNC-IEHNE--ALLEAKKM 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 19 AGEFAGMEKVGSGFGQYKVRH-----VHKTLAIKCSPLHYDREHRELLLEAKM 73
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 NLRHSRYVLLGVIIIEGKYSIYMEYMEKGNLHVLAEMSTPLSVKGRITLIEGMC 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 74 EMAKFRYILPYGIGCRE--PYGLVMEYMETGSEKLLASE-PLPMDLRFRIHETAVGMN 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 YLH--GKGVIIKDKLPENIIVNDPHIKIADLGIAFKRMSKLNNEEHNELREVDGTAKK 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 131 FLHGMSPPLHLDLKPANILLDAHVKISDFGLA-----KCGMSSHDSMDGLF-- 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 NGGLTYMAPEHLNDVNAKPEKSDVYSAFVLAITANKPEYENALICEQOLIMCISGN 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 --GTIAVLPEPRIRKESRLSDTKHDVYSAFVIMGVLTQKKPFADENILHIWKVYKGH 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 RPVDVDDITECPR---ETISIMKLCEANPEARPTFGIEKRPFFYLSOLESEVEDVK 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 RPELPYCGRAPRACSHILIRLMQRCMGODPRVTRTFEITSEIDL-CEKPDVEKTAH 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 303 SLKKEYSENNAVYKRMOSLOLDCVAVP--SSRSNATQOPGSLHSSQGLMGKPVSESNFAP 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 296 DLAHEPEKS-----SLKSEAPREPSRLKRAASAPPDNDGSLSELLSQL--DSGISQ 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 362 SLEHPOENEPSLOSGL-ODEANYHLVG-SHMDROTQOPRONAYNRE 408
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 348 TLSEPEELSRSSSGCKLPPSSSGKRLGVSVDASFSRGLSLSFERE 396
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
Q96T11 PRELIMINARY; PRT; 784 AA.
ID Q96T11;
AC Q96T11;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CDNA FLJ14518 f1s, clone NT2RM1000850, weakly similar to ankryn
DE R.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Magatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe J., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuo Y.,
RA Nihomiya K., Iwayanagi T.;
RT "NDO human cDNA sequencing project.";
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027424; BAB55102.1; -.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR001969; Aspartase_site.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; ank; 10.
DR Pfam; PF00069; pkinase; 1.

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DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS50088; ANK_REPEAT; 9.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN.1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN.1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN.1.
DR ANK_REPEAT; ATP-binding; Repeat; Transference.
KW SEQUENCE 784 AA; 86348 MW; 05B193E84E9E53AF CRC64;

Query Match
Best Local Similarity 10.94; Score 387; DB 4; Length 784;
Matches 120; Conservative 73; Mismatches 146; Indels 60; Gaps 17;

QY 14 SSDFLSEALDGGFGKVSCLFHRTQGLMKT---YKGPNC-IEHNE--ALLEAKKM 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 19 AGEFAGMEKVGSGFGQYKVRH-----VHKTLAIKCSPLHYDREHRELLLEAKM 73
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 68 NLRHSRYVLLGVIIIEGKYSIYMEYMEKGNLHVLAEMSTPLSVKGRITLIEGMC 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 74 EMAKFRYILPYGIGCRE--PYGLVMEYMETGSEKLLASE-PLPMDLRFRIHETAVGMN 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 128 YLH--GKGVIIKDKLPENIIVNDPHIKIADLGIAFKRMSKLNNEEHNELREVDGTAKK 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 131 FLHGMSPPLHLDLKPANILLDAHVKISDFGLA-----KCGMSSHDSMDGLF-- 182
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 NGGLTYMAPEHLNDVNAKPEKSDVYSAFVLAITANKPEYENALICEQOLIMCISGN 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 --GTIAVLPEPRIRKESRLSDTKHDVYSAFVIMGVLTQKKPFADENILHIWKVYKGH 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 RPVDVDDITECPR---ETISIMKLCEANPEARPTFGIEKRPFFYLSOLESEVEDVK 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 RPELPYCGRAPRACSHILIRLMQRCMGODPRVTRTFEITSEIDL-CEKPDVEKTAH 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 --DVK-----LKK-----EYSNENAVYKRMOSLOLDCVAVPS--SRN 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 300 DLDVKSPEPRSEVVPARLKRAASAPPDNDVSLSELLS--QLDSGSAVGEPEELSRSS 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 335 SATPOGSLHSSQGLMGKPVSESNFAPSLHPOENEPS 373
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 358 SESKLPSSSGKRLGVSVDASFSRGLSLSFEREPS 396
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
Q9H4D1 PRELIMINARY; PRT; 784 AA.
ID Q9H4D1;
AC Q9H4D1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protein kinase.
DE DTK.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20349657; Pubmed=10948194;
RA Baehr C., Rohrer A., Stempke L., Rinke G., Marks F., Gschwendt M.;
RT "DTK, a novel protein kinase that interacts with protein kinase
RT Cdel1. Cloning, characterization, and gene analysis.";
RL J. Biol. Chem. 275:36350-36357(2000).
DR EMBL; AJ278016; CAC04247.1; -.
DR HSSP; P25963; 11KN.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR001969; Aspartase_site.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam; PF00069; ank; 10.
DR Pfam; PF00069; pkinase; 1.

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DR InterPro: IPR002011; RTKinaseII.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00757; Furin-like; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF01030; Recep_L_domain; 2.
DR PRINTS: PR00014; ENTPEI1.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase; 1.
DR SMART: SM00060; FN3; 3.
DR SMART: SM00261; FU; 1.
DR SMART: SM00220; S_tykc; 1.
DR SMART: SM00219; TYKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; UNKNOWN_1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 1412 AA; 158944 MW; 140759FB633A3A9 CRC64;

Query Match 10.2%; Score 361.5; DB 13; Length 1412;
Best Local Similarity 28.2%; Pred. No. 1.6e-15;
Matches 125; Conservative 64; Mismatches 156; Indels 99; Gaps 19;

QY 22 ELDSGGFGKVSLOCFHRTQGL-----MIMRTVYKGPNCIEHNALLEAKMMNR 69
DB 1003 ELDSGGFGMV-----YEGLAGGVVAKDEPETRVAIKTVNESASAMREIE-FLNEASVMKE 1055

QY 70 LRHSRYVKLLGVIIEGKSYSLVMEYMEKGL--MHVLAEMST-----PLSVKGRILLIE 121
DB 1056 FNCHHVVRLGVVSOQPTLVIMELMTRGDLKSHLSLRKRENTTQVLPLKMIQWAGE 1115

QY 122 IIEGMCYLHGKGVVHDKPENILVNDHFIRKIDGLASFKMWSKLNNEHNELEVPDG 181
DB 1116 IAGMAYVLANKKRVHNDLARNQMAEDFAVKIGDGMT-----RDIYETDY 1162

QY 182 TAKKNGGTL--YMADEHLVDNAKPEKSDVYSFAVVIWAIFA-NKEPYENALICEQOLI 238
DB 1163 YRGGGGLLPVRMWSPESLKD--GVFTTMSDVMSFGVLMETATLAEPYQGSNBOYL 1220

QY 239 MCIKSG--NRPDVDITCYCPREIISLMKLCWANEAPRTPGIEKFRPFYLSOLEES 296
DB 1221 FVVEGGGLDLPD-----NCPDMLFELMRWCQYNKMRPSFLEI-----ISSIKKE 1266

QY 297 VEDDVSLKKEYSNEN-----AVYKMQSLQD-----CVAVPSRSNSGATEQ 339
DB 1267 LQSPFEMSFYEEENKPPDTEELDMVENMENIPLDPASTROPASVAAPSSCGTGTTP 1326

QY 340 PGSLSHSSQGLG-----MGVYESWFAF--SLEHPQE-----ENEP--SLQSKLD 379
DB 1327 PSAQQLSPMQGPSTPLGVPSPSSGPVASALASPGQALDKHSHGVSANGPVVLPNPND 1386

QY 380 DEANY--HLYGSRMDROTQKOPRON 402
DB 1387 EMOPYAHMNGGRKNERALLPQSS 1410

RESULT 6
Q91AA2 PRELIMINARY; PRT; 669 AA.
AC Q91AA2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Insulin-like growth factor 1 receptor 1 (Fragment).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_Taxid=7957;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=RETINA;
RA Otteson D.C., Cirenza P.F., Hitchcock P.F.;
RT "Molecular cloning and expression of igf-1 and igf-1 receptor in the
RT normal and regenerating retinas of goldfish."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: AF216772; AAF63263.1; -.
DR HSSP: P06213; 11RK.
DR InterPro: IPR007719; Euk_pkinase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR002011; RTKinaseII.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00219; TYKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
KW Glycoprotein; Phosphorylation; Receptor; Transmembrane;
KW Tyrosine-protein kinase.
FT NON TER 1
SQ SEQUENCE 669 AA; 75047 MW; 41EBB879A371000 CRC64;

Query Match 10.2%; Score 360.5; DB 13; Length 669;
Best Local Similarity 27.5%; Pred. No. 6.3e-16;
Matches 120; Conservative 60; Mismatches 154; Indels 103; Gaps 16;

QY 22 ELDSGGFGV-----SLOCFHRTQGLMIMRTVYKGGNCIEHNALLEAKMMNRLRHSV 75
DB 278 ELDSGGFGMVYEGSIAGGVAKDEPETRVAIKTVNESASLHERIE-FLNEASVMKEFNCHV 336

QY 76 VKLLGVITIEGKSYSLVMEYMEKGLMHVLAEMST-----PLSVKGRILLIEEGM 126
DB 337 VRLGVVSOQPTLVIMELMTRGDLKSHLSRASNNTSSLPPLKMIQWAGETADQM 396

QY 127 CYLHGKGVVHDKPENILVNDHFIRKIDGLASFKMWSKLNNEHNELEVPDG TAKKN 186
DB 397 AYHLAKFVRHDLARNQMAEDFVTKIGDFGT-----RDIYETDYRKGG 443

QY 187 GFTL--YMADEHLVDNAKPEKSDVYSFAVVIWAIFA-NKEPYENALICEQOLIMCIKS 243
DB 444 KGLLPVRMWSPESLKD--GVFTTMSDVMSFGVLMETATLAEPYQGSNEOYLRFVMEG 501

QY 244 G--NRPDVDITCYCPREIISLMKLCWANEAPRTPGIEKFRPFYLSOLEESVEEDY 301
DB 502 GILDKRD-----NCPDMLFELMRWCQYNKMRPSFLEI-----ISSIKDLEAGE 547

QY 302 KSLIKKEYSNENAVYKMQSLQDCAVAVPSRSNSGATEQGLSHSSQGLMGVYESWFAF 361
DB 548 KEMSFYSEEN--KEPTEELDMENV-GAMEWVPLEPSSLOP-----LAP 590

QY 362 SLEHPQE-----ENEPS--LQSKLDDEANY-H 385
DB 591 SLASPGQCAPASOGSSPPAGSSPPPPAPRTSTNSPASANGPSVWLRASFDEQOPYAH 650

QY 386 IYGSRMDROTQKOPRON 402
DB 651 MNGGRKNERALLPQSS 667

RESULT 7
Q91776 PRELIMINARY; PRT; 609 AA.
AC Q91776;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

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QY 337 TEOPGSLHSSGGLMGVPEESWFPASLE-----HQEENPESLSKLODEANYHLHYGS 389
D 1358 SLLPQS--MAEGNSQFGITETVFOFDELPLVGYDMNDEDECFISFGDDVDSSQPF 1415
QY 390 RMDQOTQO-QPQWVAANREERERRRYS--HDPFAQORPYENFQNTES----KQTVSSA 442
D 1416 MPESHSTSSVNRQPLSHQSHHNSGSEASLHNSGLIEKKPLIKKRSRQSPSPKOTIIPRP 1475
QY 443 ASHGNAVHOPSGLSOPVLYQNNGLYSSHGFTGRPLDPTAGPR--WVYRPIPSHPSL 500
D 1476 VEYLD--HGPEPLMKPD---PRSSLQNNPFSTSTADPLRGLGHNTIASSNLPGLVSR 1530
QY 501 HNIVPEPTNIGNTPTMPFSSL-----PPTDESI-----529
D 1531 PNLRLP---VLSPPPTGFKFIVSOHNSGNDNTDAGROKPPSGQPIVTHPAPLANLVHE 1587
QY 530 -KYIYSTGTGLOIAVYVMEIGTSSSLDSTNTNFKPEPAKQATFNDNTSLTDHL 587
D 1588 NELESPQATGSLSDQHT---SSTPAIATNTSSDSKSESTKSESFSLRNGLTNGHI 1642

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RESULT 9

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ID 08UW83 PRELIMINARY: PRT: 1418 AA.
AC 08UW83;

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DT 01-MAR-2002 (Tremblrel, 20, Created)
DT 01-MAR-2002 (Tremblrel, 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel, 21, Last annotation update)
DE Type 1 Insulin-like growth factor receptor.
GN FIGF-IR-2.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OC NCBI_Taxid=8255;

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RN 111
RP SEQUENCE FROM N.A.
RA Nakao N., Tanaka M., Higashimoto Y., Nakashima K.;
RT "Identification and characterization of four distinct subtypes of
RT insulin and type 1 insulin-like growth factor receptors in flounder,
RT Paralicthys olivaceus.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AB065099; BAB83670.1;
DR InterPro: IPR000494; EGFR_L_domain.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR002011; RTkinaseII.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00757; Furin-like; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRINTS: PR00104; FNTYPEIII.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00060; FN3; 3.
DR SMART: SM00261; FU; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_ITI; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1418 AA; 159651 MW; 0BA6174D2E3B2D34 CRC64;

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Query Match 9.8%; Score 346.5; DB 13; Length 1418;
 Best Local Similarity 28.5%; Pred. No. 1.6e-14;
 Matches 119; Conservative 60; Mismatches 148; Indels 91; Gaps 18;

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QY 20 SAEIDSGFGKVSICFHRTOGL-----MIKTYVKGPNCEHNEALIEPAKM 67
D 1005 SRELQGSFGMV-----YELAGVYKDEPETRVAIKTYNESASMERIE-FLNEASVM 1057
QY 68 NLRHSRYKLLGVIIIEGKSLVMEYKGNLHVLR-----AEKSTP-----LS 113
D 1058 KEFNCNHVYRLIGVSGQPTLIVIMELMTFGDLKSYLSRPRKQWSSSLPLPLKMLQ 1117
QY 114 VKGRILIEIEIGKCYLKGKVIHDKLPENLVNDNDHITADIGLAFPMWSKLNEEH 173
D 1118 MAG---QIADGMAYLANRKFVHRDLAARCMVAEDIVKIGDFGWT-----1160
QY 174 NELREVDGTAKKNGTL--YVMAPEHLDVNAKPTKSDVYSAVVAIIFA--NKEPEN 230
D 1161 RDIYETDYKRGKGGLLPVRMMSPESLKD--GVFTTSDVMSGCVYIMELSTLAEOPYG 1218
QY 231 AICQQLIMCIKSG--NRPDVDTTEYCPREIISLMKLCWEANDPAPPTPGIEKFRPF 288
D 1219 LSNQOVLRFVWEGGLEKRP-----QNCPLMTELMRMCMQYNPKMRPSFVEI-----1265
QY 289 YLSQLESVEEDVYSIKKEYSNENAVYKRNQSLQLDGV-----AVPSRSMSATDQPSLH 344
D 1266 -ISLKDLEVSFEVSEFFYSADKPSSE-QQVHLDMNDIEDVPADQPSST--QPOQAO 1321
QY 345 SSQGLGMGPVEESWFPASLEHQEENPESLSKLODEANYHLGSRMDRQTKQOPRON 402
D 1322 VPQGTTPSPSEAPAPASLS-PSSPSSPCST-----AAMDKQASQQAAN 1366

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RESULT 10

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ID 08UUY9 PRELIMINARY: PRT: 515 AA.
AC 08UUY9;

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DT 01-MAR-2002 (Tremblrel, 20, Created)
DT 01-MAR-2002 (Tremblrel, 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel, 21, Last annotation update)
DE Insulin-like growth factor I receptor (Fragment).
DE Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_Taxid=7955;

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RN 111
RP SEQUENCE FROM N.A.
RA Cheng R., Wu J.-L.;
RT "Cloning and embryonic expression of zebrafish (Danio rerio) insulin-
RT like growth factor-I receptor and its relationship with p53 tumor
RT suppressor gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY043191; AAL05594.1;
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002011; RTkinaseII.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_ITI; UNKNOWN_1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 515 AA; 57342 MW; CC28FC34AA0242D3 CRC64;

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Query Match 9.7%; Score 345.5; DB 13; Length 515;
 Best Local Similarity 27.8%; Pred. No. 4.4e-15;
 Matches 121; Conservative 56; Mismatches 160; Indels 99; Gaps 16;


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OY 22 ELDSGSGFKV-----SLCFHRTQGLMIKTYKKGNCJENHNNALLEEAKMMRLRHSRV 75
   || || || || || || || || || || || || || || || || || || || || ||
Db 127 ELGGSFGGVYEGIAKGVKKDEPTRVAKTKYTNESLHERIE-FLNEASVMEKFCNHHV 185
   || || || || || || || || || || || || || || || || || || || || ||
OY 76 VKLLGVITIEEGKYSLWMEYMEKGNIMHVLKAEINST-----PLSVGRILLIETIEGM 126
   || || || || || || || || || || || || || || || || || || || || ||
Db 186 VRLLEGVWSOGOPTLWIMEIMLTQDLKSYLRSLRSVENTSSLPRLPKKMIQMGELADGM 245
   || || || || || || || || || || || || || || || || || || || || ||
OY 127 CYLHGKGVIHMDLAKRENIILYDNDPHIKXINDLGLASKKMSKLNNEHNELREVDGTAKKN 186
   || || || || || || || || || || || || || || || || || || || || ||
Db 246 AYLNNKFEVHRDLAARNCVAAEDFVTKIGDFGNT-----RDIEFDYVRKGG 292
   || || || || || || || || || || || || || || || || || || || || ||
OY 187 GGTL--YMADEHLNDVNAKPTREKSDVYSFAVLNIAIFA-NKEPEYNALCEODLIMCITS 243
   || || || || || || || || || || || || || || || || || || || || ||
Db 293 KGLLPVRMRMSPSLND--GVFTTMSDVMSFGVYLMIATLAEPRYOGMSMEQVLYRRVMEG 350
   || || || || || || || || || || || || || || || || || || || || ||
OY 244 G--NRPDVDDITETCPRELLISMLKLCWEANPEARPTPGIEEKKFRFPYLSQLEESVEDY 301
   || || || || || || || || || || || || || || || || || || || || ||
Db 351 GULDPPD-----NCPDMLFELMRMCWQYNPKMRPSEFLI-----ISSIKEDLEAGF 386
   || || || || || || || || || || || || || || || || || || || || ||
OY 302 KSLKKEYSENENAVVRMOSLOLDCVAVPSSRSASATEOGSLHSOGGLMGPRVEESWEAP 361
   || || || || || || || || || || || || || || || || || || || || ||
Db 397 KETSFYEESEN--KRPTEELDMENV-GTMEVNPRLPSSSLOP-----LAP 439
   || || || || || || || || || || || || || || || || || || || || ||
OY 362 SLEHPE-----ENEPSSLOKLQDEANHYLGSRMDRQTKOOPRONVAYNREEE 410
   || || || || || || || || || || || || || || || || || || || || ||
Db 440 SISPPQOCTAAAGSCSPSPSPSPS-----STDKHPLPTSAANGPS- 481
   || || || || || || || || || || || || || || || || || || || || ||
OY 411 RRRRVSHDPFMOQRPY 426
   || || || || || || || || || || || || || || || || || || || || ||
Db 482 ---WVLRGPFPEGOPY 494
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RESULT 11
001700
ID 001700 PRELIMINARY; PRF: 855 AA.
AC 001700.
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-MAR-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 95.1 kDa protein F33E2.2.
GN F33E2.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP Lennard N.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AL0022593; CAI18635.2; -.
DR EMBL: Z84574; CAI18635.2; JOINED.
DR EMBL: Z84574; CAB06544.2; -.
DR EMBL: AL022593; CAB06544.2; JOINED.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR InterPro: IPR004040; Sry_Pkinase.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00221; STYCK; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
KW transerase.
SQ SEQUENCE 855 AA; 95786 MW; F44DD2538CB7D95A CRC64;

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OY 13 KSSD-----ELESADGSGFGXKSLCFHROGIMIKITVYKPCNCEJHEALLE-EAK 65
Db 49 KSDEIEMELDPDAISLEWLGSSGCAV---RGOLENRV-----ARKVNOJKEFEIK 1000
OY 66 MMRRLHRSRVKLLGVLIEEGYSVLMEVMEKGNIMHVLKAEKSTPLSVGRILLETIEG 1250
Db 101 HLMHRIKHOINTELGLGSCSPCYCIYMEGCSGOLCTYLSKRSNTITRELFQAWKELADG 1600
OY 126 MCLYHKGVLHKLDPENTLVNDNFHICLADLGASFKMMSKLNNEEHELREVDGTAKK 1850
Db 161 MHYLIHQNVKVIHRDKSPNLIISAEDSIKIDEGTSHM-----KKMDSTVMS 2070
OY 186 NGSTLYYMAPEHLNDVNAKP-TEKSDVSVFVAVLITATANKERPEMAICEDOLIMCTKSG 2440
Db 208 FCGTGVMAPEM---TKOPCEKEDVYVSFGVVLMEMLTRETPRYAN-IAQMAITFGVTN 2630
OY 245 --NRPPVDITTECSEPIISLMKLOMEANPEARPFEGIE---EKPRFVLSOLE--- 2950
Db 264 ILSLP---MPEARPGVLVLLIKOCSLOKGRNRPSFSHIRONHWEIPELFEMTEEBWOL 3190
OY 296 -----SVEDEVKSLKEEYSNENAVVKMOJLODCV 3260
Db 320 AMDSYREFAKCIQIPESTYTRHDCGRKSAFAMEEELQKRHHOLNHIINDIRMYEMKL--- 3760
OY 327 AVPSRNSNATDEPGSLHSSOGILGMGPEESWFALEHPOENERPSLOSKLODEANYHL 3860
Db 377 ---KRTKNMYDXLOCSFTLEKIKESLEAE-WEKDLTEREOMHNONSPKAAVAPRAOLRG 4310
OY 387 YGSR----MDROTKOOPRONAVN-REEFRRRRVSHDFPAOQRYENFQNTIEGKGYSS 4410
Db 432 YPNEGVDMDSDDEDVPCRGSPYRCNSNTSSSGVQSSPFSRO---SSRSASGOOTRSE 4480
OY 442 AA-----SHGNVHQPGLTS-----4570
Db 489 GANPKRLRMDAIRHSGSWEIETLGCAKRGSPADSCFSODSCMSHAGACSTAINGGCOY 5480
OY 458 -QBOVLUYON-NGLYSSHGFR-----PLDPOTA--GPRVWY-PRIPSHMPSLNI---P 5040
Db 549 CYSQOTLYRMNGDQWMSGRIASRRRVSTYKNSKTAVAPQGFPTDPSRNV--HGVISS 6060
OY 505 VPETNVLGNTPTWPESSLP-----PTDESIKYTYIYNSTGIGIQAIVNWEIG 5500
Db 607 SPSSSKLNSYSVRNAPHOLEDGCCCAHARAPAKSLAVM-----6490
OY 551 GTSSSLDSTNTNFKPEPAKQALFNDNTTSLDKHNDPIENGLK 596
Db 650 -TSSS-----RARSPTPYDNDFEANAESPVDDESPKNLKEK 685

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	RESULT	12	
DR	013064		
ID	013064	PRELIMINARY;	PRT; 488 AA.
AC	013064;		
DT	01-JUL-1997 (Tremblrel, 04, Created)		
DT	01-JUL-1997 (Tremblrel, 04, last sequence update)		
DT	01-MAR-2002 (Tremblrel, 20, last annotation update)		
DE	Lyn protein tyrosine kinase..		
GN	LYN.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Ampiphbia; Batrachia; Anura; Mesobatrachia; Pipidoae; Pipidae;		
CC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Fukami Y., Funabiki K., Sato K.;		
RT	"Nucleotide sequence of Xenopus Lyn protein tyrosine kinase."		
RL	Submitted (APR-1997) to the EMBL/Genebank/DBJ databases.		
CC	- I - SIMILARITY: CONTAINS 1 SH3 DOMAIN.		
DR	EMBL: AB003358; BAA20078.1; -		
DR	HSPD; P08631; IAD5.		
DR	InterPro: IPR000719; Euk_pkinase.		
DR	Interpro: IPR000980; SH2.		

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa S., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 DR EMBL: AK013606; BAB28926.1; -
 DR HSSP: P11362; 1FGK.
 DR MGD: MGI:99259; Matk.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk.pkinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYRKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_APP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding; Transferase.
 SQ .SEQUENCE 465 AA; 51615 MW; 8CB0A4CB7CAB9F CRC64;

Query Match 9.5%; Score 338.5; DB 11; Length 465;
 Best Local Similarity 33.6%; Pred. No. 1.1e-14;
 Matches 90; Conservative 46; Mismatches 99; Indels 33; Gaps 10;

Y 21 AELDSGCGFVSLCFHRTGGLMI-MKTVYKGPICIEHNEALLBEAKMMRLRSRYVKLL 79
 Db 197 AQLGEGEFQAV-----LOGEYLGQVAVAKNIKCDVTAQAFIDETAVMKRLQHRNLRVRL 250

Y 80 GVIIIEGKYSLVMEYMEKGNLMHLAKEMSTPLSVKG--RIIEIEGKCYLHGKGVIRK 137
 Db 251 GVILHNGLY-IYWEHVSCKGLVNFELTRGRALVYSTQLOLQALHVAEGMEYLESKLVHR 309

Y 138 DLKPENILVNDNFHIADIGLASFQWMSKLNNEEHNELEVDGTAKKNGTLYYAPPEH 197
 Db 310 DLARNILVSEDLVAVKVSDFGLAK-----AERKGLDSSRL---PVKWTAPEA 353

Y 198 LNDVNAKPKTEKSVYSFAVVAIFA-NKEPYENALCEOOLLICISGNRPVDDITTEYC 256
 Db 354 LK--NGRFSSKSDVSWSEFGLVLEVFYSYGRAPYK-MSLKEVSEAVKGYRMEPPD---GC 407

Y 257 PREIISLKLCEANPEARPTFGIEEK 284

Db 408 PGSVHTLMSCWMEAPARRPFRKIYEK 435

RESULT 15
 ID P70223 PRELIMINARY; PRT; 465 AA.
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE HYL tyrosine kinase.
 GN MATK OR HYLTK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA x C57BL/6; TISSUE=EMBRYONIC STEM;
 RX MEDLINE=96280730; PubMed=8694808;
 RA Hamaguchi I., Yamaguchi N., Suda J., Iwama A., Hirao A., Hashiyama M.,
 RA Aizawa S.I., Suda T.,
 RT "Analysis of CSK homologous kinase (CHK/HYL) in hematopoiesis by
 RT utilizing gene knockout mice."
 RT Biochem. Biophys. Res. Commun. 224:172-179(1996).
 CC -1-SIMILARITY: CONTRAINS 1 SH3 DOMAIN.
 DR EMBL: X83972; CAA58806.1; -
 DR HSSP: P11362; 1FGK.
 DR MGD: MGI:99259; Matk.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000001; Euk.pkinase; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYRKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_APP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ .SEQUENCE 465 AA; 51571 MW; 24C2DBA71A08A3B9 CRC64;

Query Match 9.5%; Score 338.5; DB 11; Length 465;
 Best Local Similarity 33.6%; Pred. No. 1.1e-14;
 Matches 90; Conservative 46; Mismatches 99; Indels 33; Gaps 10;

Y 21 AELDSGCGFVSLCFHRTGGLMI-MKTVYKGPICIEHNEALLBEAKMMRLRSRYVKLL 79
 Db 197 AQLGEGEFQAV-----LOGEYLGQVAVAKNIKCDVTAQAFIDETAVMKRLQHRNLRVRL 250

Y 80 GVIIIEGKYSLVMEYMEKGNLMHLAKEMSTPLSVKG--RIIEIEGKCYLHGKGVIRK 137
 Db 251 GVILHNGLY-IYWEHVSCKGLVNFELTRGRALVYSTQLOLQALHVAEGMEYLESKLVHR 309

Y 138 DLKPENILVNDNFHIADIGLASFQWMSKLNNEEHNELEVDGTAKKNGTLYYAPPEH 197
 Db 310 DLARNILVSEDLVAVKVSDFGLAK-----AERKGLDSSRL---PVKWTAPEA 353

Y 198 LNDVNAKPKTEKSVYSFAVVAIFA-NKEPYENALCEOOLLICISGNRPVDDITTEYC 256
 Db 354 LK--NGRFSSKSDVSWSEFGLVLEVFYSYGRAPYK-MSLKEVSEAVKGYRMEPPD---GC 407

Y 257 PREIISLKLCEANPEARPTFGIEEK 284

Thu Jun 26 09:21:39 2003

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Page 10

DB 408 PGSVHTLMGSCWEAPARRPPRRKIVEK 435

Search completed: June 21, 2003, 16:14:48
Job time : 90 secs

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Db      1 MOPDMSLVNIKMKSSDFLESALDGGFGKVSICFHRTQGLMIMKTVYKGPNCIEHNEAL 60
QY      61 LEEAKMMNRRLRHSRVYKLLGVYIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Db      61 LEEAKMMNRRLRHSRVYKLLGVYIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
QY      121 EIEEGMCTYLGKGVYHKDLKPEKNIIVDNDHFHKTADGLASFKMSKLNNEEHNELEVD 180
Db      121 EIEEGMCTYLGKGVYHKDLKPEKNIIVDNDHFHKTADGLASFKMSKLNNEEHNELEVD 180
QY      181 GTAKNGSTLYYMAPEHLNDVNAKPTKESDVYSEAVVLMALFANKPEYENALCEQOLIMC 240
Db      181 GTAKNGSTLYYMAPEHLNDVNAKPTKESDVYSEAVVLMALFANKPEYENALCEQOLIMC 240
QY      241 IKSGRNPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKRPFTYLSQLEESVED 300
Db      241 IKSGRNPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKRPFTYLSQLEESVED 300
QY      301 VKSLKKEYSNENAVYKRMQSLQDLCVAVPSRSNSATQPGSLHSSQGLGMGPVEESMFA 360
Db      301 VKSLKKEYSNENAVYKRMQSLQDLCVAVPSRSNSATQPGSLHSSQGLGMGPVEESMFA 360
QY      361 PSLEHPOEENPSLOSQLODEANVHLYGSRMDROTQOOPRONVAYNREERRRRVSHDPF 420
Db      361 PSLEHPOEENPSLOSQLODEANVHLYGSRMDROTQOOPRONVAYNREERRRRVSHDPF 420
QY      421 AQORRYENFQNTTEGKGTIVYSSAASHGNAVHOPSGLTQPOVLYONNGLYSSHGFTRPDL 480
Db      421 AQORRYENFQNTTEGKGTIVYSSAASHGNAVHOPSGLTQPOVLYONNGLYSSHGFTRPDL 480
QY      481 PGTAGPRVWYRPIPSHMSLNINIVPETNYLGNPTMPFSSLPPTDESIRKTYINSGTIO 540
Db      481 PGTAGPRVWYRPIPSHMSLNINIVPETNYLGNPTMPFSSLPPTDESIRKTYINSGTIO 540
QY      541 IGAYNMEIGTSSSLDSTNTNKEEPAKYOALFNDTSLTDKHLDPITRENLGKHMKN 600
Db      541 IGAYNMEIGTSSSLDSTNTNKEEPAKYOALFNDTSLTDKHLDPITRENLGKHMKN 600
QY      601 CARKLGFTQSOIDEIDHDYERDGLKEKYOMLOKVMREGIKGATVGLAQLHOCSTRID 660
Db      601 CARKLGFTQSOIDEIDHDYERDGLKEKYOMLOKVMREGIKGATVGLAQLHOCSTRID 660
QY      661 LLSLIIVYSON 671
Db      661 LLSLIIVYSON 671

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RESULT 2
US-08-444-005-17
: Sequence 17, Application US/08444005
: Patent No. 5674734
: GENERAL INFORMATION:
: APPLICANT: Leder, Phillip
: APPLICANT: Seed, Brian
: APPLICANT: Stanger, Ben Z.
: APPLICANT: Lee, Tae-Ho
: APPLICANT: Kim, Emily
: TITLE OF INVENTION: CELL DEATH PROTEIN
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street, Suite 3100
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/444,005

```

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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00383/026001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-005-17

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Query Match          99.5%; Score 3529; DB 1; Length 709;
Best Local Similarity 99.6%; Pred. No. 1.5e-284;
Matches 668; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db      1 MOPDMSLVNIKMKSSDFLESALDGGFGKVSICFHRTQGLMIMKTVYKGPNCIEHNEAL 60
QY      61 LEEAKMMNRRLRHSRVYKLLGVYIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Db      61 LEEAKMMNRRLRHSRVYKLLGVYIEEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
QY      121 EIEEGMCTYLGKGVYHKDLKPEKNIIVDNDHFHKTADGLASFKMSKLNNEEHNELEVD 180
Db      121 EIEEGMCTYLGKGVYHKDLKPEKNIIVDNDHFHKTADGLASFKMSKLNNEEHNELEVD 180
QY      181 GTAKNGSTLYYMAPEHLNDVNAKPTKESDVYSEAVVLMALFANKPEYENALCEQOLIMC 240
Db      181 GTAKNGSTLYYMAPEHLNDVNAKPTKESDVYSEAVVLMALFANKPEYENALCEQOLIMC 240
QY      241 IKSGRNPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKRPFTYLSQLEESVED 300
Db      241 IKSGRNPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKRPFTYLSQLEESVED 300
QY      301 VKSLKKEYSNENAVYKRMQSLQDLCVAVPSRSNSATQPGSLHSSQGLGMGPVEESMFA 360
Db      301 VKSLKKEYSNENAVYKRMQSLQDLCVAVPSRSNSATQPGSLHSSQGLGMGPVEESMFA 360
QY      361 PSLEHPOEENPSLOSQLODEANVHLYGSRMDROTQOOPRONVAYNREERRRRVSHDPF 420
Db      361 PSLEHPOEENPSLOSQLODEANVHLYGSRMDROTQOOPRONVAYNREERRRRVSHDPF 420
QY      421 AQORRYENFQNTTEGKGTIVYSSAASHGNAVHOPSGLTQPOVLYONNGLYSSHGFTRPDL 480
Db      421 AQORRYENFQNTTEGKGTIVYSSAASHGNAVHOPSGLTQPOVLYONNGLYSSHGFTRPDL 480
QY      481 PGTAGPRVWYRPIPSHMSLNINIVPETNYLGNPTMPFSSLPPTDESIRKTYINSGTIO 540
Db      481 PGTAGPRVWYRPIPSHMSLNINIVPETNYLGNPTMPFSSLPPTDESIRKTYINSGTIO 540
QY      541 IGAYNMEIGTSSSLDSTNTNKEEPAKYOALFNDTSLTDKHLDPITRENLGKHMKN 600
Db      541 IGAYNMEIGTSSSLDSTNTNKEEPAKYOALFNDTSLTDKHLDPITRENLGKHMKN 600
QY      601 CARKLGFTQSOIDEIDHDYERDGLKEKYOMLOKVMREGIKGATVGLAQLHOCSTRID 660
Db      601 CARKLGFTQSOIDEIDHDYERDGLKEKYOMLOKVMREGIKGATVGLAQLHOCSTRID 660
QY      661 LLSLIIVYSON 671
Db      661 LLSLIIVYSON 671

```

RESULT 3

US-08-444-005-15
: Sequence 15, Application US/08444005
: Patent No. 5674734
: GENERAL INFORMATION:
: APPLICANT: Leder, Philip
: APPLICANT: Seed, Brian
: APPLICANT: Stanger, Ben Z.
: APPLICANT: Lee, Tae-Ho
: APPLICANT: Kim, Emily
: TITLE OF INVENTION: CELL DEATH PROTEIN
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street, Suite 3100
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/444,005
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,164
: REFERENCE/DOCKET NUMBER: 00383/026001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 656 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-444-005-15

Query Match 68.4% Score 2423.5; DB 1; Length 656;
Best Local Similarity 69.8%; Pred. No. 8.4e-193;
Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

QY 1 MOPMSLNVIRKMSDDLESALDSDGSGFGKYSICFHRTOGLIMIKTYKGFNCIEHNEAL 60
DB 1 MOPMSLNDIKMASSDLEKTDSDGSGFGKYSICYHSHGFIILKKYITGPNRAEYEV 60
QY 61 LEEAKMMNRRLHSHRVKLLGVIIIEGKYSIYMEYMEKGNLMHVLKAEMSTPLSVKGRILL 120
DB 61 LEEAKMMNRRLHSHRVKLLGVIIIEGKYSIYMEYMEKGNLMHVLKTDVPLSLKGRITV 120
QY 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLSAFKMMSKLNNEHNEHLEVD 180
DB 121 EAIIGCMCYLHDKGVIIHDKLPENTLVNDPFIKTIADGLSAFKMMSKLNNEHNEHLEVD 180
QY 181 GTAKK-NGGTLTYAAPRLNDVNAKPTKESDVSFAVYLAIFANKEPEYENATEOOLIM 239
DB 181 STTKKNGGTLTYAAPRLNDVNAKPTKESDVSFAVYLAIFANKEPEYENATEOOLIM 239
QY 240 CIRKGNRPDVDDITETCPRETIISLMKLCWEANPEARPTFGIEKFRPFYLSOLEEVEE 299
DB 241 CIRKGNRPVVEIETCPRETIISLMERKQWAIPEDRPTFLGIEEFREFYLSHPEEYEE 300
QY 300 DVKSLKKEYSNNAAVVRMSQLQDCAVAVSSRSNSATEOPGSLHSSOGLGMGVEESWF 359
DB 301 DVASLAKKEYPDQSPVLQRMFSLQHDCAVPLPSPRSNS--EOPGSLHSSOGLGMGVEESWF 358
QY 360 APSLEHPOEENEPISLOKLODEANYHLXGSRMDROTQOPQONVAAYNNEERRRRVSHDP 419

DB 359 SSSEPEYDDENDREVSQAKLOEASVYHAFGICFAEKQTPQPRQNAAYNNEERKRVRSHDP 418
QY 420 FAQORPEYENFONTEGKGTVSSAASHGNVAHQPSGLTSQPOVLYONNGLYSHGFGTRPL 479
DB 419 FAQORARENIKASAGARCHSDSTSRGIAVOQLSWPATO---TWNNGNLVHQGF----- 470
QY 480 DPGTAGPRVWYRPIPSHNPISLHNIIPVETNVLGNTPTMPRESSLPPTDESIXYTYINSGI 539
DB 471 -GTTGCGWYPPNLSQWYSTYKTPVPETNIPGSTPMPYFSGVADDLKTYTFNSGI 528
QY 540 QIGAVYWEIIGTSSSLDSTNTNFKPEPAKVOAIDNTSLTDKHLDPREMIGKHWK 599
DB 529 QIGHNHYMDVGLNS---QPPNNCKREBSTSRHQAIDNTSLTDHLNPIREMLGQWK 584
QY 600 NCARKLGFTSQIDEIDHDERDGLKEKYYOMLOKMWREGIKATGYKLAQALHQCRI 659
DB 585 NCARKLGFTESQIDEIDHDERDGLKEKYYOMLOKMWREGIKATGYKLAQALHQCRI 644
QY 660 DLLSLTYVSON 671
DB 645 DLLNHLIRASQS 656

RESULT 4
US-09-069-023-28
: Sequence 28, Application US/09069023A
: Patent No. 6348573
: GENERAL INFORMATION:
: APPLICANT: Nunez, Gabriel
: APPLICANT: Inohara, Naohiro
: APPLICANT: Koseki, Takeyoshi
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
: FILE REFERENCE: UM-03333
: CURRENT APPLICATION NUMBER: US/09/069,023A
: CURRENT FILING DATE: 1998-04-27
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO: 28
: LENGTH: 656
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-069-023-28

Query Match 68.4% Score 2423.5; DB 4; Length 656;
Best Local Similarity 69.8%; Pred. No. 8.4e-193;
Matches 469; Conservative 70; Mismatches 116; Indels 17; Gaps 5;

QY 1 MOPMSLNVIRKMSDDLESALDSDGSGFGKYSICFHRTOGLIMIKTYKGFNCIEHNEAL 60
DB 1 MOPMSLNDIKMASSDLEKTDSDGSGFGKYSICYHSHGFIILKKYITGPNRAEYEV 60
QY 61 LEEAKMMNRRLHSHRVKLLGVIIIEGKYSIYMEYMEKGNLMHVLKAEMSTPLSVKGRILL 120
DB 61 LEEAKMMNRRLHSHRVKLLGVIIIEGKYSIYMEYMEKGNLMHVLKTDVPLSLKGRITV 120
QY 121 EIIIGCMCYLHKGVIHDKLPENTLVNDPFIKTIADGLSAFKMMSKLNNEHNEHLEVD 180
DB 121 EAIIGCMCYLHDKGVIIHDKLPENTLVNDPFIKTIADGLSAFKMMSKLNNEHNEHLEVD 180
QY 181 GTAKK-NGGTLTYAAPRLNDVNAKPTKESDVSFAVYLAIFANKEPEYENATEOOLIM 239
DB 181 STTKKNGGTLTYAAPRLNDVNAKPTKESDVSFAVYLAIFANKEPEYENATEOOLIM 239
QY 240 CIRKGNRPDVDDITETCPRETIISLMKLCWEANPEARPTFGIEKFRPFYLSOLEEVEE 299
DB 241 CIRKGNRPVVEIETCPRETIISLMERKQWAIPEDRPTFLGIEEFREFYLSHPEEYEE 300
QY 300 DVKSLKKEYSNNAAVVRMSQLQDCAVAVSSRSNSATEOPGSLHSSOGLGMGVEESWF 359
DB 301 DVASLAKKEYPDQSPVLQRMFSLQHDCAVPLPSPRSNS--EOPGSLHSSOGLGMGVEESWF 358


```

: Sequence 5, Application US/09329418
: Patent No. 6096539
:
: GENERAL INFORMATION:
:
: APPLICANT: ZENECA Limited
:
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
:
: FILE REFERENCE: PHM.70536
:
: CURRENT APPLICATION NUMBER: US/09/329,418
:
: CURRENT FILING DATE: 1999-06-11
:
: NUMBER OF SEQ. ID NOS: 39
:
: SOFTWARE: FASTSEQ for Windows Version 3.0
:
: SEQ ID NO 5
:
: LENGTH: 518
:
: TYPE: PRT
:
: ORGANISM: Dattificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Dominant Negative Mutant Embodiment
:
: US-09-329,418-5

```

Query Match	12.28	Score 433	DB 3	Length 518
Best Local Similarity	25.58	Pred. NO. 1.2e-27		
Matches 146	Conservative 96	Mismatches 184	Indels 146	Gaps 22

QY	1	SSOFSSAEL-DSSGSGKXSLCFHRTQGLMTIKTYKGRNCLENHEALLBEAKMKNLRH	72
Db	17	STLEELNQELVKGKGGTVFRAOHKRWG-----YDAVAVRYNSKALSREVKAMASIDN	69
QY	73	SRVVKLLGTV-----IEEGKYSILAMEYMEKGNLMHVLKAEKSTPLSYVGRILILIGMC	127
Db	70	EFLRLREGVLEKVMQDPKRALYVTKFMEKNSLSLLOSCPRRPLLCRLKEVYLGME	129
QY	128	YLHGKG-VIHKDKPENILVNDHFIRIKIADLGASAFKMSKLNNEHNEHLEVDGAK-	184
Db	130	YLEDQNPVLLRHRLKPSNVLLDPELVKVLADGLSTFGGSGQ-----SGTSGG	177
QY	185	KNGSTLYUAMPBLNDVNAKPTREKSDVYSFAVYLAITANKE---PYE-----NAIEEQ	236
Db	178	EPGGTIGTAYLPVNVNKKASTASDVYSGFLMAVYLAGVELPEPRLSYBAVCNRQ	237
QY	237	LIMCIKSGNRPDVDDITTEYCPRE-----IISLMKLCWEANEARPTF---PGIEEKRFP	287
Db	238	-----NRPSLAEPLQAGPEPTPGLEGELKELMOJCWSSPEKDRSPQECPLKDEYFQ-	288
QY	288	FYLSQLEESVEEDYKSLKEKEYENENAVYKRMOSLOLDCVAVPSSRSNSATEQPSLHSSQ	347
Db	289	-----WVENNNNAVSVZKDFLSQLTSSNRRF-----STIPES-----	320
QY	348	GLGMGVVEESWFAPSLEHPOEENEPSSLOSKLODEANYHLYLSRMDROTQOQPRQNVAYNR	407
Db	321	--GOGGTEDMGCFRRTIENOSHRRNDVWVSEWL-----NKLNLLEPSSVKKC	365
QY	408	EE-ERRRRYSHDPFAQGRPYENFQNTGEGKGYVSSAASHGNAVHQPSSLTSQPOVLYQN	466
Db	366	PSLTKRSRAQEEVYQA-----WTAGTSSSMAOP---PQTPETSTFRN	406
QY	467	GLYSSHGEGTRPLDPECTAGPRVWYKRPDSHMSPLHNIPVETNYLGNTPTVWFSSLPD	526
Db	407	QMPSS-----PTSTGT-----PS-----PGPRGNOGAEROGMWSCTRRP	441
QY	527	ESLK-----YTIYNSGICIQAGNAVMEIGTSS	554
Db	442	NPVTGPRPLVNIYSGVGVNNYVLTMOQTAA	473

```

RESULT 8
US-09-531-914-3
: Sequence 3: Application US/09531914
: Patent No. 6267956
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/531,914
: CURRENT FILING DATE: 2000-03-21

```

```

? PRIOR APPLICATION NUMBER: 09/329,418
? PRIOR FILING DATE: 1999-06-11
? NUMBER OF SEQ ID NOS: 39
? SOFTWARE: FASTSEQ for windows Versio
? SEQ ID NO 3
? LENGTH: 318
? TYPE: PRT
? ORGANISM: Homo Sapiens
? OS-09-531-914-3

```

Query Match	12.28;	Score 433;	DB 4;	Length 518;
Best Local Similarity	25.58;	Pred. NO. 1.2e-27;		
Matches 146;	Conservative 96;	Mismatches 184;	Indels 146;	Gaps 22

```

QY      14 SDFPLESABL -DSGGGKYSCLCFHRTQGLMTKTYTKKPCNLEINHEALLBEAKMMNLRH 72
Db      17 STEELNEQELVKGKGGVTFRAQHRKMG-----YDAVAVIKVSKALSREVKAMASLDN 69
QY      73 SRVVKLLGVY-----IEEGKYSALVMEYMEKGNLHVLKAEKSTPSTLVYGRITLIEIGMC 127
Db      70 EFLVRLREGVLEKYNMQDCKPALVYTKFEMNSGLSSLOSCPRRWPILCRLLKEVYLGMF 129
QY      128 YLHGKG--VIHKDLAEENILVDNDEPHIKIADLGLASFPMKSKLNEEHEHLEVDGYAK- 184
Db      130 YLHDNDPVLHLRDLKPSNVLLDPELHVYKLAQFGLSTFGGSGO-----SGYGSQ 177
QY      185 KNGGTLYMAPELHNDVNAKPTREKSDVYSFAVLAIFANKE---PYE-----NAICEQ 236
Db      178 EPGGTGLYLAPELFVNVNKRKASTADVYSFGILMAVLAAGREVELPELPSTLYEAVCNMQ 237
QY      237 LINCISGNRPDDVDITTEYCPRE-----IISLMKLWEANDEARPTF---PGIEEKFRP 287
Db      238 -----NRPSTLAELPQAGPEPTPGLEGKLKELMQLCWMSSEKDPQECJLPKTXDEVFQ- 288
QY      288 FYLSOLEESVEDVDYKLTKEYSNENAVYKRMQSLQDLCVAVPSSKSNATQEPQSLHSQ 347
Db      289 -----WBNNNNAVSYVYKFLSLQKSSNRRF-----SLPES----- 320
QY      348 GLCMGPVESWFAFSLPHEDENEPSLKLQDEANVHLVYGRMDROTQOPRONVAYNR 407
Db      321 --GQGTENDMGFRTTEINGHSRNDVYSEML-----NKLWLEPPSSVYKKC 365
QY      408 EE-ERRRRVSHDPFAQGRYENFQMTKEGCTGYSSAASHGNAVYHQPSGLTSQPVLYXONN 466
Db      366 PSTLTKSRQOEEDVPOA-----WTAGTSSMAQOP--PQPTPTSTFRN 406
QY      467 GLYSHGFGTRPLDPTAGPRVYRPRIPSHMPSLHNIVPPTNLGNTPWTFSSLPPTD 526
Db      407 QMS-----PSTST-----PS-----PGPRNGCAERQGNMNSCRTPR 441
QY      527 ESIRK---YTIYNSTGIGIGAVNYEIGTSS 554
Db      442 NPVTGRPLVNIYNCSGVGVGDNNYLTMOOTTA 473

RESULT 9
US-09-531-914-5
: Sequence 5, Application US/09531914
: Patent No. 6267956
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM 70536
: CURRENT APPLICATION NUMBER: US/09/531,914
: CURRENT FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 09/329,418
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 5
: LENGTH: 518
: TYPE: PRT
: ORGANISM: Dafticial Sequence

```

```
; FEATURE:
; OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-5
```

Query Match	12.2%	Score 433	DB 4	Length 518
Best Local Similarity	25.5%	Pred. No. 1.2e-27		
Matches 146; Conservative	96	Mismatches 184	Indels 146	Gaps 22

[illegible]

```

RESULT 10
US-09-329-418-9
, Sequence 9, Application US/09329418
, Patent No. 6036539
, GENERAL INFORMATION:
, APPLICANT: ZENECA Limited
, TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
, FILE REFERENCE: PHM 70536
, CURRENT APPLICATION NUMBER: US/09/329,418
, CURRENT FILING DATE: 1999-06-11
, NUMBER OF SEQ ID NOS: 39
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 9
, LENGTH: 518
, TYPE: PRT
, ORGANISM: Artificial Sequence
FEATURE:
, OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-9

```

Query Match	12.28;	Score 432;	DB: 3;	Length 518;
Best Local Similarity	24.38;	Pred. No. 1.4e-27;		
Matches 144:	Conservative	91;	Mismatches	171;
			Indels	186;
			Gaps	20

```

OY 14 SDELTSABL -DSGFGKXSLCFHHTOGIMTKVYKGPNCIENENALLBEAKMNRJRH 72
Db 17 STELENEOLVCKGGGVTFRAOHKKWC-----YDVAKYTKSAISEVYKAMASLDN 69
OY 73 SRVYKLGVY----FEEGKYSLWMEYMEKGLNHLVLAKESTPLSKGJILIEIEGMC 127
Db 70 EFLVRLRGVIEKKNMOPDKPALVYKRFPMENSSLSLSSLOOCPRPWPLPLCLLKEVLYGMC 129
OY 128 YLHGKG-VIHKDKLENILVDNDFHIKIDAGLASFKMSKLNNEEHNELEVDGTAK- 184
Db 130 YLHDONFVLLHRLPKPSNVLLDPELHVYKLADFGSLTFGGSGO-----SGTSGO 177
OY 185 KNGSTLYAMPEHLNDVNAKPTREKSDVYSFAVVAIAIPANE---PYE-----NALCEOO 236
Db 178 EPGGTGGLYLAPELVVNAKKASTADSVSGILIMAVLAGREVELPTEPSLYEAYCANKRO 237
OY 237 LIMICKSNRPDDVDDITEYCPRE-----IISLMKLWMEANBEARPTF---PGLEEKFRP 287
Db 238 -----NRPSLAELPQAGPPELPGLEGELKELMOJCWSSPEKKDPRSQBELPRTDFQ- 288
OY 288 FYLSQEESEVEDYKSLKREYSENAVYKRMOSLOLDCVAVPPSSRSNATEDPQSLHSSO 347
Db 289 -----MVENNNAVSVTKDELSQLRSSNRRF-----SIPES----- 350
OY 348 GLGMPVEEBSWFAPSLEHPEENE-----PSL--OSKLDDA 382
Db 321 --GOGGTGEMDFRRTTENOSHNRDVAWSFWLKLNLLEBPSSVYKKCCSLTKRRAOEEO 378
OY 383 NYHLYSGRMDQRKOOPRONAVAYNBEERERRRVSHDPAOORPYENFONTEGKGTVYSSA 442
Db 379 VPQWMTAGTSSDSMAQRPQT-----PENSFRNQMPSPSTSGNPSPG----- 420
OY 443 ASHGNAVHOPSGILTSOPVLYONNGLLSYSHGCTRPRLDPGTAGRPVWTRPLPSHPSLHN 502
Db 421 -PRNOQAEBOGMNA-----S 435
OY 503 IVPETNYLONTPTMPFSSLPPTDESIKTYIYNSGIGIOGAVNYMEIGTSS 554
Db 436 CRPEPBPVIGRPVY-----NITNCSGVGVGNNTLLIMOOTTA 473

```

```

Result 11
US-09-531-914-9
; Sequence 9, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531,914
; CURRENT FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-9

```

Query Match	12.2%	Score 432	DB 4	Length 518
Best Local Similarity	24.3%	Pred. No. 1.4e-27		
Matches 144: Conservative	91	Mismatches 171	Indels 186	Gaps 20

QY 14 SSDLDESAEL-DSGGFKVSLCFHRQGLMIKTYKGCNLEENHALLBEAKMKNLRH 72
 :
Dd 17 SIETLENDELVGKGFTFVRADRRWG-----YDAVKIVNSKAISREVKAMASIDN 69
 :
QY 73 SRVKKLGVI-----IEEGKYSLYMEYMKEGNIMHVLAEMSTPLSVNGRIILEIIIGMC 127
 :

Db 70 EFVLRLEGVIEKVMDDPKPALVTYKPMENGLSLGLOSQCPRPWPLLCRLKEEVLGMF 129
QY 128 YLHGKG--VIHKDLKPEILVDNDPHIKIADLGLASFPMKSKLNNEEHNEELREVDGTAK- 184
Db 130 YLHQNPNVLLHRLKPSNVLLDPELHVKLADFGSLSTFGGSGQ-----SGTSGS 177
QY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVLMATFANKE---PYE-----NAICEQ 236
Db 178 EPGGTGLIAPLAEFLVNNRKAASDVSFGLIMMAYLAGREVELPTEPSPLYEAVCNRQ 237
QY 237 LIMIKSGNRPDVDITIEYCPRE-----IISLMKLCWEANEARPTF---PGIEKFRP 287
Db 238 -----NRSIAELPQAGPETGLBLKELMOLCWSSEPKDRPSFOECLPKTDEVFQ- 288
QY 288 FYLSOLESEVEDYKSLKKEYSNENAVYKRMQSLQLODVAAPSSRSNATQPSLSHSQ 347
Db 289 -----MVENNMAAVSTYKDFLSQLRSSNRF-----STPES----- 320
QY 348 GLGMPVEESWAFSLLEHPOEENE-----PSL--QSKLODEA 382
Db 321 --GGGTGEMDGFRTIENQHSRNDVVMSEMLKINLEPSPSSVPKCKPSLKRSAOEQ 378
QY 383 NYHLGSRMDRQTKOQPRONAVYNRBERRRRVSHDPAQORPYENFQTEGKTIVYSSA 442
Db 379 VPAWMTAGTSSDSMAQPPQT-----PETSTFRNQMPSTSTGTPSPG----- 420
QY 443 ASHGNAVHQPSGLTSQPVLYQNNGLYSSHGFTRPIDPGTACGRVWYRPIPSHMPSLHN 502
Db 421 -PRNQAEROGMNA-----S 435
QY 503 IPVEPTVYLGNTPTMPFSSLPPTDESIKYTYINSTGIOIGAYNMEIGTSS 554
Db 436 CRTEPNPNYGRPLV-----NINCSGVQVGDNNYLTMOQTAA 473

RESULT 12
US-09-329-418-4
; Sequence 4, Application US/09329418
; Patent No. 6096539
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/329,418
; CURRENT FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-4

Query Match 12.0%; Score 425; DB 3; Length 518;
Best Local Similarity 25.3%; Pred. No. 5.4e-27;
Matches 145; Mismatches 185; Indels 146; Gaps 22;

QY 14 SSDPLESAEL-DSGFGKVSICFHRTQGLMIMKTVYKGPNCIEHNEALLEEAKMNNRLRH 72
Db 17 STEELNDELVGKGGFGTVFRAQHRKMG-----YDAVAVTVSKAISREVKAMASLDN 69
QY 73 SRVKKLGLV-----IEGKYSVMEYMEKGNLHVLAEMNSTPLSVKGRILIEIIGMC 127
Db 70 EFVLRLEGVIEKVMDDPKPALVTYKPMENGLSLGLOSQCPRPWPLLCRLKEEVLGMF 129
QY 128 YLHGKG--VIHKDLKPEILVDNDPHIKIADLGLASFPMKSKLNNEEHNEELREVDGTAK- 184
Db 130 YLHQNPNVLLHRLKPSNVLLDPELHVKLADFGSLSTFGGSGQ-----SGTSGS 177
QY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVLMATFANKE---PYE-----NAICEQ 236
Db 178 EPGGTGLIAPLAEFLVNNRKAASDVSFGLIMMAYLAGREVELPTEPSPLYEAVCNRQ 237

Db 178 EPGGTGLIAPLAEFLVNNRKAASDVSFGLIMMAYLAGREVELPTEPSPLYEAVCNRQ 237
QY 237 LIMIKSGNRPDVDITIEYCPRE-----IISLMKLCWEANEARPTF---PGIEKFRP 287
Db 238 -----NRSIAELPQAGPETGLBLKELMOLCWSSEPKDRPSFOECLPKTDEVFQ- 288
QY 288 FYLSOLESEVEDYKSLKKEYSNENAVYKRMQSLQLODVAAPSSRSNATQPSLSHSQ 347
Db 289 -----MVENNMAAVSTYKDFLSQLRSSNRF-----STPES----- 320
QY 348 GLGMPVEESWAFSLLEHPOEENEPSLSQLODEANVLYGSRMDRQTKOQPRONAVYNR 407
Db 321 --GGGTGEMDGFRTIENQHSRNDVVMSEMLKINLEPSPSSVPKCKPSLKRSAOEQ 365
QY 408 EE-ERRRVSHDPAQORPYENFQTEGKTIVYSSASHGNAVHQPSGLTSQPVLYQN 466
Db 366 PSLKRSAOEQVQA-----WTAGTSSDSMAQPPQTPEPSTFRN 406
QY 467 GLYSSHGFTRPIDPGTACGRVWYRPIPSHMPSLHNIPVEPTVYLGNTPTMPFSSLPPTD 526
Db 407 QMPS-----PTSTGT-----PS-----PGRNGAEROGMNSCRTPPEP 441
QY 527 ESIR---YTYINSTGIOIGAYNMEIGTSS 554
Db 442 NPVTGRPLVNIYNCGVQVGDNNYLTMOQTAA 473

RESULT 13
US-09-531-914-4
; Sequence 4, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531,914
; CURRENT FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-4

Query Match 12.0%; Score 425; DB 4; Length 518;
Best Local Similarity 25.3%; Pred. No. 5.4e-27;
Matches 145; Conservative 96; Mismatches 185; Indels 146; Gaps 22;

QY 14 SSDPLESAEL-DSGFGKVSICFHRTQGLMIMKTVYKGPNCIEHNEALLEEAKMNNRLRH 72
Db 17 STEELNDELVGKGGFGTVFRAQHRKMG-----YDAVAVTVSKAISREVKAMASLDN 69
QY 73 SRVKKLGLV-----IEGKYSVMEYMEKGNLHVLAEMNSTPLSVKGRILIEIIGMC 127
Db 70 EFVLRLEGVIEKVMDDPKPALVTYKPMENGLSLGLOSQCPRPWPLLCRLKEEVLGMF 129
QY 128 YLHGKG--VIHKDLKPEILVDNDPHIKIADLGLASFPMKSKLNNEEHNEELREVDGTAK- 184
Db 130 YLHQNPNVLLHRLKPSNVLLDPELHVKLADFGSLSTFGGSGQ-----SGTSGS 177
QY 185 KNGGTLVYMAPEHLNDVNAKPTKSDVYSFAVLMATFANKE---PYE-----NAICEQ 236
Db 178 EPGGTGLIAPLAEFLVNNRKAASDVSFGLIMMAYLAGREVELPTEPSPLYEAVCNRQ 237
QY 237 LIMIKSGNRPDVDITIEYCPRE-----IISLMKLCWEANEARPTF---PGIEKFRP 287
Db 238 -----NRSIAELPQAGPETGLBLKELMOLCWSSEPKDRPSFOECLPKTDEVFQ- 288

```

QY 288 FYLSQLESVEEDYKSLKKEYSNENAVYKRMOSTLOLDCVAVPSSRSNATEPOGSLHSSQ 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 -----MVENNMAAAVSTVADFLSOLRSSNRFE-----SIPES-----320
QY 348 GLGMPVEESWFAVSLRQENEPESLOSRLQDEANTHLYSRRMDROTQOOPRONVAYNR 407
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 321 --GGGTMDGFRRTIENQHSRNDVWVSEWL-----NKLNLPEPSSVRKCC 365
QY 408 EE-ERRRVSHPDPAQRPYENFQTEGKGTIVSSAASHGNAVQPSGLTSQPOLVYONN 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 366 PSIFRRAQEEQVQA-----WTAGTSSDMAOP---PQTPETSPFRN 406
QY 467 GLYSHGCTRLPDGTGPRVWRPPIPSHNPISLHNITVPETNLGNTPMPFSSLPPTD 526
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 407 QMPS-----PTSTGT-----PS---GPRGNOGAEROGMWSCTRPDP 441
QY 527 ESIR-----YTIYNSGIGIAGVNYWMEIGTSS 554
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 442 NPVTGRPLVNIYICSGVQVGDNNYITMQTTA 473

```

```

RESULT 14
US-09-329-418-8
; Sequence 8, Application US/09329418
; Patent No. 6096539
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/329,418
; CURRENT FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Delta Death Domain
US-09-329-418-8

```

```

Query Match 11.7%; Score 414; DB 3; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-26;
Matches 124; Conservative 77; Mismatches 129; Indels 110; Gaps 16;

QY 14 SSDPLESAEL-DSGGFGKVSICFHRTQGLMIMKTYKGPNCIEHNEALLEAKMNRRLH 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 17 STEELENOELVKGKGFVFRQHRKMG-----YDVAVKIVNSKAISREVKAMASLDN 69
QY 73 SRVVKLLGVITIEG-----KSLVMEYMEKGNLMHVAKAEMSTPLSVKGRITILEIEGM 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 EFLVRLGVIEKVGSSODPKPALVTKEFENGSLSGLOSCPPRPWPLLCRLIKEVVLGM 129
QY 127 CYLHGKG--VIHKDLKPNILVNDNFHIKIDGLASFKMSKLNNEHNEHLREVDTAK 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 FYLHDQNPVLLHRDLKPSNVLLDPELHVKLADFGISTFGGSGQ-----SGTGS 177
QY 185 -KNGGLTYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKE---PYE-----NAICQ 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 GEGGGLGYLAPLELFVNNRKAStADSVYSFGILMAVLAGREVELPTEPSLYEAVCNR 237
QY 236 OLIMCKSGNRPVDVDTIEYCPRE-----IISLMLCKEANPEARPTF---PGIEEKR 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 Q-----NRSIALFLPQAGETPTEGLKELMQLCWSSEPKDRSPFOECLPKTDEVFQ 289
QY 287 PFYLSQLESVEEDYKSLKKEYSNENAVYKRMOSTLOLDCVAVPSSRSNATEPOGSLHSS 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 290 -----MVENNMAAAVSTVKDFLSOLRSSNRFE-----SIPES-----321
QY 347 QGLGMPVEESWFAVSLRQENEPESLOSRLQDEANTHLYSRRMDROTQOOPRONVAYNR 407
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 --GGGTMDGFRRTIENQHSRNDVWVSEWL-----NKLNLPEPSSVRKCC 365

```

```

QY 382 ANYHLYGSRMDROTQOOPRQ 401
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 379 QVPOAMTAGTSSDMAOPQ 398

```

```

Query Match 11.7%; Score 414; DB 4; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-26;
Matches 124; Conservative 77; Mismatches 129; Indels 110; Gaps 16;

```

```

QY 14 SSDPLESAEL-DSGGFGKVSICFHRTQGLMIMKTYKGPNCIEHNEALLEAKMNRRLH 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 17 STEELENOELVKGKGFVFRQHRKMG-----YDVAVKIVNSKAISREVKAMASLDN 69
QY 73 SRVVKLLGVITIEG-----KSLVMEYMEKGNLMHVAKAEMSTPLSVKGRITILEIEGM 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 EFLVRLGVIEKVGSSODPKPALVTKEFENGSLSGLOSCPPRPWPLLCRLIKEVVLGM 129
QY 127 CYLHGKG--VIHKDLKPNILVNDNFHIKIDGLASFKMSKLNNEHNEHLREVDTAK 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 FYLHDQNPVLLHRDLKPSNVLLDPELHVKLADFGISTFGGSGQ-----SGTGS 177
QY 185 -KNGGLTYMAPEHLNDVNAKPTKSDVYSFAVVLMAIFANKE---PYE-----NAICQ 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 GEGGGLGYLAPLELFVNNRKAStADSVYSFGILMAVLAGREVELPTEPSLYEAVCNR 237
QY 236 OLIMCKSGNRPVDVDTIEYCPRE-----IISLMLCKEANPEARPTF---PGIEEKR 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 Q-----NRSIALFLPQAGETPTEGLKELMQLCWSSEPKDRSPFOECLPKTDEVFQ 289
QY 287 PFYLSQLESVEEDYKSLKKEYSNENAVYKRMOSTLOLDCVAVPSSRSNATEPOGSLHSS 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 290 -----MVENNMAAAVSTVKDFLSOLRSSNRFE-----SIPES-----321
QY 347 QGLGMPVEESWFAVSLRQENEPESLOSRLQDEANTHLYSRRMDROTQOOPRONVAYNR 407
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 322 --GGGTMDGFRRTIENQHSRNDVWVSEWL-----NKLNLPEPSSVRKCC 365
QY 379 QVPOAMTAGTSSDMAOPQ 398

```

Search completed: June 21, 2003, 16:16:12
Job time : 29 secs


```

Db      361 PSLEHPOEENPSLOSLODEANANYHLGSRMDROTQOOPRONVAYNREERRRVSHDPF 420
Qy      421 AOOPEYENFONTEGKTAVYSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFTRPJD 480
      421 AOOPEYENFONTEGKTAVYSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFTRPJD 480
Db      421 AOOPEYENFONTEGKTAVYSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFTRPJD 480
Qy      481 PGTAGPRVWYRPIPSHMPSLHNI PVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
      481 PGTAGPRVWYRPIPSHMPSLHNI PVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
Db      481 PGTAGPRVWYRPIPSHMPSLHNI PVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
Qy      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHMKN 600
      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHMKN 600
Db      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHMKN 600
Qy      601 CARLKGFTQSOIDEIDHDERDGLKEKYOMLOKVMREGIKGATVGLAOLHOCSTRID 660
      601 CARLKGFTQSOIDEIDHDERDGLKEKYOMLOKVMREGIKGATVGLAOLHOCSTRID 660
Db      601 CARLKGFTQSOIDEIDHDERDGLKEKYOMLOKVMREGIKGATVGLAOLHOCSTRID 660
Qy      661 LLSSLIYVSQN 671
      661 LLSSLIYVSQN 671
Db      661 LLSSLIYVSQN 671

```

RESULT 2

```

US-60-452-680-20110
; Sequence 20110, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GROPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20110
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-20110

```

```

Query Match      99.9%: Score 3541; DB 7; Length 671;
Best Local Similarity 99.9%: Pred. No. 4.2e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MOPDMSLVNIKKSSDFLESALDSDGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
      1 MOPDMSLVNIKKSSDFLESALDSDGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
Db      1 MOPDMSLVNIKKSSDFLESALDSDGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
Qy      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Db      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Qy      121 EIIEMCYLHGKGYIHKDLKPENLIVNDPHIKIADGLASFMMKSKLNNEHNELREVD 180
      121 EIIEMCYLHGKGYIHKDLKPENLIVNDPHIKIADGLASFMMKSKLNNEHNELREVD 180
Db      121 EIIEMCYLHGKGYIHKDLKPENLIVNDPHIKIADGLASFMMKSKLNNEHNELREVD 180
Qy      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSAFVAVLMAIFANKEPEYENALICEQOLIMC 240
      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSAFVAVLMAIFANKEPEYENALICEQOLIMC 240
Db      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSAFVAVLMAIFANKEPEYENALICEQOLIMC 240
Qy      241 IKSNGRPVDVDDITEYCPREIISLMKLCWEANPEARPTFGIEEKRFPYLSOLEESVEED 300
      241 IKSNGRPVDVDDITEYCPREIISLMKLCWEANPEARPTFGIEEKRFPYLSOLEESVEED 300
Db      241 IKSNGRPVDVDDITEYCPREIISLMKLCWEANPEARPTFGIEEKRFPYLSOLEESVEED 300
Qy      301 VKSJLKEYSNENAVYKRMQSLQDLQVAVPSRSNSATQPGSLSSOGLMGVPEESWFA 360
      301 VKSJLKEYSNENAVYKRMQSLQDLQVAVPSRSNSATQPGSLSSOGLMGVPEESWFA 360
Db      301 VKSJLKEYSNENAVYKRMQSLQDLQVAVPSRSNSATQPGSLSSOGLMGVPEESWFA 360
Qy      361 PSLEHPOEENPSLOSLODEANANYHLGSRMDROTQOOPRONVAYNREERRRVSHDPF 420
      361 PSLEHPOEENPSLOSLODEANANYHLGSRMDROTQOOPRONVAYNREERRRVSHDPF 420
Db      361 PSLEHPOEENPSLOSLODEANANYHLGSRMDROTQOOPRONVAYNREERRRVSHDPF 420

```

```

Qy      421 AOOPEYENFONTEGKTAVYSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFTRPJD 480
      421 AOOPEYENFONTEGKTAVYSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFTRPJD 480
Db      421 AOOPEYENFONTEGKTAVYSSAASHGNNAVHOPSGLTSPQVLYXONNGLYSSHGFTRPJD 480
Qy      481 PGTAGPRVWYRPIPSHMPSLHNI PVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
      481 PGTAGPRVWYRPIPSHMPSLHNI PVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
Db      481 PGTAGPRVWYRPIPSHMPSLHNI PVETNYLGNFTMPFSSLPPTDESICKYTYNSTG10 540
Qy      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHMKN 600
      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHMKN 600
Db      541 IGAAYNMEIGTSSSLDSTNTNFKKEEPAKYOALFDNTTSLTDKHLDP1RENLGKHMKN 600
Qy      601 CARLKGFTQSOIDEIDHDERDGLKEKYOMLOKVMREGIKGATVGLAOLHOCSTRID 660
      601 CARLKGFTQSOIDEIDHDERDGLKEKYOMLOKVMREGIKGATVGLAOLHOCSTRID 660
Db      601 CARLKGFTQSOIDEIDHDERDGLKEKYOMLOKVMREGIKGATVGLAOLHOCSTRID 660
Qy      661 LLSSLIYVSQN 671
      661 LLSSLIYVSQN 671
Db      661 LLSSLIYVSQN 671

```

RESULT 3

```

US-60-455-444-6356
; Sequence 6356, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6356
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-455-444-6356

```

```

Query Match      99.9%: Score 3541; DB 7; Length 671;
Best Local Similarity 99.9%: Pred. No. 4.2e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MOPDMSLVNIKKSSDFLESALDSDGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
      1 MOPDMSLVNIKKSSDFLESALDSDGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
Db      1 MOPDMSLVNIKKSSDFLESALDSDGFGKVSICFHRTOGLIMIKTYKGPNCIEHNAL 60
Qy      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Db      61 LEEAKMMNRRLHRSRYVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
Qy      121 EIIEMCYLHGKGYIHKDLKPENLIVNDPHIKIADGLASFMMKSKLNNEHNELREVD 180
      121 EIIEMCYLHGKGYIHKDLKPENLIVNDPHIKIADGLASFMMKSKLNNEHNELREVD 180
Db      121 EIIEMCYLHGKGYIHKDLKPENLIVNDPHIKIADGLASFMMKSKLNNEHNELREVD 180
Qy      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSAFVAVLMAIFANKEPEYENALICEQOLIMC 240
      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSAFVAVLMAIFANKEPEYENALICEQOLIMC 240
Db      181 GTAKKNGSTLYYMAPEHLNDVNAKPTKSDVYSAFVAVLMAIFANKEPEYENALICEQOLIMC 240
Qy      241 IKSNGRPVDVDDITEYCPREIISLMKLCWEANPEARPTFGIEEKRFPYLSOLEESVEED 300
      241 IKSNGRPVDVDDITEYCPREIISLMKLCWEANPEARPTFGIEEKRFPYLSOLEESVEED 300
Db      241 IKSNGRPVDVDDITEYCPREIISLMKLCWEANPEARPTFGIEEKRFPYLSOLEESVEED 300
Qy      301 VKSJLKEYSNENAVYKRMQSLQDLQVAVPSRSNSATQPGSLSSOGLMGVPEESWFA 360
      301 VKSJLKEYSNENAVYKRMQSLQDLQVAVPSRSNSATQPGSLSSOGLMGVPEESWFA 360
Db      301 VKSJLKEYSNENAVYKRMQSLQDLQVAVPSRSNSATQPGSLSSOGLMGVPEESWFA 360
Qy      361 PSLEHPOEENPSLOSLODEANANYHLGSRMDROTQOOPRONVAYNREERRRVSHDPF 420
      361 PSLEHPOEENPSLOSLODEANANYHLGSRMDROTQOOPRONVAYNREERRRVSHDPF 420
Db      361 PSLEHPOEENPSLOSLODEANANYHLGSRMDROTQOOPRONVAYNREERRRVSHDPF 420

```

```

QY 421 AAOQRYENFONTECKGTAVYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
    |||||||
Db 421 AAOQRYENFONTECKGTAVYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
QY 481 PGTAGPRVWTRPIPSHMPSLHNIPVETNTLGNTPMPFSSLPPTDESIKTYINSGIG 540
    |||||||
Db 481 PGTAGPRVWTRPIPSHMPSLHNIPVETNTLGNTPMPFSSLPPTDESIKTYINSGIG 540
QY 541 IGAVNMEIGTSSLDSTNTNFKKEPAKYOAIPONTTSLDQKHLDPITRENGKHKMN 600
    |||||||
Db 541 IGAVNMEIGTSSLDSTNTNFKKEPAKYOAIPONTTSLDQKHLDPITRENGKHKMN 600
QY 601 CARLGTQSOIDEIDHDYERDGLKEKVVOMLQKWVREGIKGATVGLAQAALHQCGRID 660
    |||||||
Db 601 CARLGTQSOIDEIDHDYERDGLKEKVVOMLQKWVREGIKGATVGLAQAALHQCGRID 660
QY 661 LLSLIYVSON 671
    |||||||
Db 661 LLSLIYVSON 671

```

RESULT 4

```

US-60-465-241-6356
: Sequence 6356, Application US/60465241
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: C1001468
: CURRENT APPLICATION NUMBER: US/60/465, 241
: CURRENT FILING DATE: 2003-04-23
: NUMBER OF SEQ. ID NOS: 258418
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6356
: LENGTH: 671
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-465-241-6356

```

```

Query Match          99.9%: Score 3541; DB 7; Length 671;
Best Local Similarity 99.9%: Pred. No. 4.2e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MOPDMSLVITKMKSSDFLESALDSGGFGKVSICFHRTOGLIMKTYKGPNCIEHNEAL 60
    |||||||
Db 1 MOPDMSLVITKMKSSDFLESALDSGGFGKVSICFHRTOGLIMKTYKGPNCIEHNEAL 60
QY 61 LEEAKMMNRLRHSRVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
    |||||||
Db 61 LEEAKMMNRLRHSRVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
QY 121 EIIEGMCYLLHGKGVIAHKDLKPENLVNDNDFHIKTIADGLASFWMKSKLNNEEHNELEVD 180
    |||||||
Db 121 EIIEGMCYLLHGKGVIAHKDLKPENLVNDNDFHIKTIADGLASFWMKSKLNNEEHNELEVD 180
QY 181 GTAKKNGCTLYYMAPEHLNDVNAKPTKESDVYSFAVVLMAIFANKKEYENAIICQOOLIMC 240
    |||||||
Db 181 GTAKKNGCTLYYMAPEHLNDVNAKPTKESDVYSFAVVLMAIFANKKEYENAIICQOOLIMC 240
QY 241 IKSGRNPDDVDITCYCPREITISLMKLCMEANPEARPTFGIEEKFREFYLSOLEEVEED 300
    |||||||
Db 241 IKSGRNPDDVDITCYCPREITISLMKLCMEANPEARPTFGIEEKFREFYLSOLEEVEED 300
QY 301 VKSILKKEYSNEANVVKRMOSLQDLCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 360
    |||||||
Db 301 VKSILKKEYSNEANVVKRMOSLQDLCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 360
QY 361 PSLEHPOEENPESLOSLODEANVHLGSRMDROTQKQPRONAVYNEEERRRRVSHDPF 420
    |||||||
Db 361 PSLEHPOEENPESLOSLODEANVHLGSRMDROTQKQPRONAVYNEEERRRRVSHDPF 420
QY 421 AAOQRYENFONTECKGTAVYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
    |||||||

```

```

Db 421 AAOQRYENFONTECKGTAVYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
    |||||||
QY 481 PGTAGPRVWTRPIPSHMPSLHNIPVETNTLGNTPMPFSSLPPTDESIKTYINSGIG 540
    |||||||
Db 481 PGTAGPRVWTRPIPSHMPSLHNIPVETNTLGNTPMPFSSLPPTDESIKTYINSGIG 540
QY 541 IGAVNMEIGTSSLDSTNTNFKKEPAKYOAIPONTTSLDQKHLDPITRENGKHKMN 600
    |||||||
Db 541 IGAVNMEIGTSSLDSTNTNFKKEPAKYOAIPONTTSLDQKHLDPITRENGKHKMN 600
QY 601 CARLGTQSOIDEIDHDYERDGLKEKVVOMLQKWVREGIKGATVGLAQAALHQCGRID 660
    |||||||
Db 601 CARLGTQSOIDEIDHDYERDGLKEKVVOMLQKWVREGIKGATVGLAQAALHQCGRID 660
QY 661 LLSLIYVSON 671
    |||||||
Db 661 LLSLIYVSON 671

```

RESULT 5

```

US-60-443-566-4424
: Sequence 4424, Application US/60443566
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: C1001447
: CURRENT APPLICATION NUMBER: US/60/443, 566
: CURRENT FILING DATE: 2003-01-30
: NUMBER OF SEQ. ID NOS: 25102
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4424
: LENGTH: 821
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-443-566-4424

```

```

Query Match          99.9%: Score 3541; DB 7; Length 821;
Best Local Similarity 99.9%: Pred. No. 5.5e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MOPDMSLVITKMKSSDFLESALDSGGFGKVSICFHRTOGLIMKTYKGPNCIEHNEAL 60
    |||||||
Db 151 MOPDMSLVITKMKSSDFLESALDSGGFGKVSICFHRTOGLIMKTYKGPNCIEHNEAL 210
QY 61 LEEAKMMNRLRHSRVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 120
    |||||||
Db 211 LEEAKMMNRLRHSRVVLLGVIIIEGKYSLVMEYMEKGNLMHVLKAEKSTPLSVKGRITL 270
QY 121 EIIEGMCYLLHGKGVIAHKDLKPENLVNDNDFHIKTIADGLASFWMKSKLNNEEHNELEVD 180
    |||||||
Db 271 EIIEGMCYLLHGKGVIAHKDLKPENLVNDNDFHIKTIADGLASFWMKSKLNNEEHNELEVD 330
QY 181 GTAKKNGCTLYYMAPEHLNDVNAKPTKESDVYSFAVVLMAIFANKKEYENAIICQOOLIMC 240
    |||||||
Db 331 GTAKKNGCTLYYMAPEHLNDVNAKPTKESDVYSFAVVLMAIFANKKEYENAIICQOOLIMC 390
QY 241 IKSGRNPDDVDITCYCPREITISLMKLCMEANPEARPTFGIEEKFREFYLSOLEEVEED 300
    |||||||
Db 391 IKSGRNPDDVDITCYCPREITISLMKLCMEANPEARPTFGIEEKFREFYLSOLEEVEED 450
QY 301 VKSILKKEYSNEANVVKRMOSLQDLCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 360
    |||||||
Db 451 VKSILKKEYSNEANVVKRMOSLQDLCVAVPSSRSNSATEOPGSLHSSOGLGMPVEESWFA 510
QY 361 PSLEHPOEENPESLOSLODEANVHLGSRMDROTQKQPRONAVYNEEERRRRVSHDPF 420
    |||||||
Db 511 PSLEHPOEENPESLOSLODEANVHLGSRMDROTQKQPRONAVYNEEERRRRVSHDPF 570
QY 421 AAOQRYENFONTECKGTAVYSSAASHGNAVHQPSSLTQPOVLYONNGLYSHGFGTRPLD 480
    |||||||

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Db 571 A00REYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTGPLD 630
Qy 481 PGTAGPRWYRPIPSHMPSLNINIPVETNYLGNPTMPFSSLPPTDESIXTYINSTGIG 540
Db 631 PGTAGPRWYRPIPSHMPSLNINIPVETNYLGNPTMPFSSLPPTDESIXTYINSTGIG 690
Qy 541 IGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDMTSLTDKHLDPIRENLGKHMKN 600
Db 691 IGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDMTSLTDKHLDPIRENLGKHMKN 750
Qy 601 CARLIGFTQSOIDEIDH0YERDGLKEKYOMLQKWMEGKIGATVGLA0ALH0CSRID 660
Db 751 CARLIGFTQSOIDEIDH0YERDGLKEKYOMLQKWMEGKIGATVGLA0ALH0CSRID 810
Qy 661 LLSLIYVS0N 671
Db 811 LLSLIYVS0N 821

RESULT 6
US-60-452-680-20112
: Sequence 20112, Application US/60452680
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: GROPE, Andrew
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: CLO01450
: CURRENT APPLICATION NUMBER: US/60/452,680
: CURRENT FILING DATE: 2003-03-07
: NUMBER OF SEQ ID NOS: 116213
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 20112
: LENGTH: 821
: TYPE: PRF
: ORGANISM: Homo sapiens
US-60-452-680-20112

Query Match 99.9%; Score 3541; DB 7; Length 821;
Best Local Similarity 99.9%; Pred. No. 5.5e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MOPDMSLVYIKKSSDPLESAELDSGFGKVSICFHRTOGLIMTKTYKGCNCTEHNEL 60
Db 151 MOPDMSLVYIKKSSDPLESAELDSGFGKVSICFHRTOGLIMTKTYKGCNCTEHNEL 210
Qy 61 LEEAKMNRRLRHSRVYKLLGVYIEEGKYSLVMEYKEGNLHVLKAEKSTPLSVKGRITL 120
Db 211 LEEAKMNRRLRHSRVYKLLGVYIEEGKYSLVMEYKEGNLHVLKAEKSTPLSVKGRITL 270
Qy 121 EIEGMCYLHGKGVTHKDLKPEINILVNDPFHKTADLGLASFKMSKLNNEHNELREVD 180
Db 271 EIEGMCYLHGKGVTHKDLKPEINILVNDPFHKTADLGLASFKMSKLNNEHNELREVD 330
Qy 181 GTAKKNGGTLYYMAPEHNDVNAKPTKESDVYSFAVYLMALFANKEPEENALICE00LIMC 240
Db 331 GTAKKNGGTLYYMAPEHNDVNAKPTKESDVYSFAVYLMALFANKEPEENALICE00LIMC 390
Qy 241 IKSGRNPVDVDTTECPREIISLMKLCWEANPEARPTPGIIEKFRPYLSQLEESVED 300
Db 391 IKSGRNPVDVDTTECPREIISLMKLCWEANPEARPTPGIIEKFRPYLSQLEESVED 450
Qy 301 VKSLKKEYSNENAVVYKRM0SLQDCVAVPSSRSNSAT0PGSLHSS0GLGMPVEESWFA 360
Db 451 VKSLKKEYSNENAVVYKRM0SLQDCVAVPSSRSNSAT0PGSLHSS0GLGMPVEESWFA 510
Qy 361 PSLEH0EENEPESL0SKLQDEANHYLHYSRMDR0TK00PR0NVAVYNNREERRRVSHPF 420
Db 511 PSLEH0EENEPESL0SKLQDEANHYLHYSRMDR0TK00PR0NVAVYNNREERRRVSHPF 570
Qy 421 A00RPEYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTGPLD 480
Db 571 A00RPEYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTGPLD 630

Qy 481 PGTAGPRWYRPIPSHMPSLNINIPVETNYLGNPTMPFSSLPPTDESIXTYINSTGIG 540
Db 631 PGTAGPRWYRPIPSHMPSLNINIPVETNYLGNPTMPFSSLPPTDESIXTYINSTGIG 690
Qy 541 IGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDMTSLTDKHLDPIRENLGKHMKN 600
Db 691 IGAVNYMEIGTSSSLDSTNTNFKKEEPAKYOALFDMTSLTDKHLDPIRENLGKHMKN 750
Qy 601 CARLIGFTQSOIDEIDH0YERDGLKEKYOMLQKWMEGKIGATVGLA0ALH0CSRID 660
Db 751 CARLIGFTQSOIDEIDH0YERDGLKEKYOMLQKWMEGKIGATVGLA0ALH0CSRID 810
Qy 661 LLSLIYVS0N 671
Db 811 LLSLIYVS0N 821

RESULT 7
US-60-455-444-6358
: Sequence 6358, Application US/60455444
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: CLO01455
: CURRENT APPLICATION NUMBER: US/60/455,444
: CURRENT FILING DATE: 2003-03-18
: NUMBER OF SEQ ID NOS: 50986
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6358
: LENGTH: 821
: TYPE: PRF
: ORGANISM: Homo sapiens
US-60-455-444-6358

Query Match 99.9%; Score 3541; DB 7; Length 821;
Best Local Similarity 99.9%; Pred. No. 5.5e-274;
Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MOPDMSLVYIKKSSDPLESAELDSGFGKVSICFHRTOGLIMTKTYKGCNCTEHNEL 60
Db 151 MOPDMSLVYIKKSSDPLESAELDSGFGKVSICFHRTOGLIMTKTYKGCNCTEHNEL 210
Qy 61 LEEAKMNRRLRHSRVYKLLGVYIEEGKYSLVMEYKEGNLHVLKAEKSTPLSVKGRITL 120
Db 211 LEEAKMNRRLRHSRVYKLLGVYIEEGKYSLVMEYKEGNLHVLKAEKSTPLSVKGRITL 270
Qy 121 EIEGMCYLHGKGVTHKDLKPEINILVNDPFHKTADLGLASFKMSKLNNEHNELREVD 180
Db 271 EIEGMCYLHGKGVTHKDLKPEINILVNDPFHKTADLGLASFKMSKLNNEHNELREVD 330
Qy 181 GTAKKNGGTLYYMAPEHNDVNAKPTKESDVYSFAVYLMALFANKEPEENALICE00LIMC 240
Db 331 GTAKKNGGTLYYMAPEHNDVNAKPTKESDVYSFAVYLMALFANKEPEENALICE00LIMC 390
Qy 241 IKSGRNPVDVDTTECPREIISLMKLCWEANPEARPTPGIIEKFRPYLSQLEESVED 300
Db 391 IKSGRNPVDVDTTECPREIISLMKLCWEANPEARPTPGIIEKFRPYLSQLEESVED 450
Qy 301 VKSLKKEYSNENAVVYKRM0SLQDCVAVPSSRSNSAT0PGSLHSS0GLGMPVEESWFA 360
Db 451 VKSLKKEYSNENAVVYKRM0SLQDCVAVPSSRSNSAT0PGSLHSS0GLGMPVEESWFA 510
Qy 361 PSLEH0EENEPESL0SKLQDEANHYLHYSRMDR0TK00PR0NVAVYNNREERRRVSHPF 420
Db 511 PSLEH0EENEPESL0SKLQDEANHYLHYSRMDR0TK00PR0NVAVYNNREERRRVSHPF 570
Qy 421 A00RPEYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTGPLD 480
Db 571 A00RPEYENF0NTEGKGTAYSSAASHGNAVH0PSGLTSP0VLY0NNGLYSSHGFGTGPLD 630


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Db      481 YMEIGTSSLLDSTNTNFKKEEPAKYQAI FDNNTSLDKHLDP IRENIGKHKNCARL 540
Qy      606 GFTQSQIDEIDHDYERDGLKEKYOMLQKWMREGIGATVGKLAQALHQC SRIDLSSL 665
Db      541 GFTQSQIDEIDHDYERDGLKEKYOMLQKWMREGIGATVGKLAQALHQC SRIDLSSL 600
Qy      666 IYVSON 671
Db      601 IYVSON 606

RESULT 10
US-60-452-680-20111
; Sequence 20111, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20111
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-20111

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Query Match      90.4%; Score 3204; DB 7; Length 606;
Best Local Similarity 99.8%; Pred. No. 3.1e-247;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      66 MMNRLRHSRVYKLLGVIIEEGKYSLVMEYMEKGNLMHVLKAKMSTPLSVKRIILEIEG 125
Db      1 MMNRLRHSRVYKLLGVIIEEGKYSLVMEYMEKGNLMHVLKAKMSTPLSVKRIILEIEG 60
Qy      126 MCVLHGKGVIRKDLKPENILVNDNFHRIADLGLASFWMKSKLNNEEHNEELREVDGTAKK 185
Db      61 MCVLHGKGVIRKDLKPENILVNDNFHRIADLGLASFWMKSKLNNEEHNEELREVDGTAKK 120
Qy      186 NGCTLYMAPHLNDVNAKPTKESDVYSFAVVLNAIFANKPEYENALICEOOLIMCISGN 245
Db      121 NGCTLYMAPHLNDVNAKPTKESDVYSFAVVLNAIFANKPEYENALICEOOLIMCISGN 180
Qy      246 RPDVDITEYCPRREIISLMKLCWEANPEARPTFGIEEKFPRFYLSQLEESVEEDVSKL 305
Db      181 RPDVDITEYCPRREIISLMKLCWEANPEARPTFGIEEKFPRFYLSQLEESVEEDVSKL 240
Qy      306 KEYSNENAVVRKMSQLODCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWFAPSLEH 365
Db      241 KEYSNENAVVRKMSQLODCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWFAPSLEH 300
Qy      366 POENEPBSLOKLODEANYHLXGSRMDROTQORONAVAYNREBERRRRVSHDFFAQR 425
Db      301 POENEPBSLOKLODEANYHLXGSRMDROTQORONAVAYNREBERRRRVSHDFFAQR 360
Qy      426 YENFONTEGKGTVYSSAASHGNAVHOPSGLTQPOVLYONNGLYSSHGFGTRPLDPTAG 485
Db      361 YENFONTEGKGTAVSSAASHGNAVHOPSGLTQPOVLYONNGLYSSHGFGTRPLDPTAG 420
Qy      486 PRVWRPRLPSPHPSLHNIPVPEETNYLGNTPMPFSSLPPTDESICKYITYNSTGIGICAYN 545
Db      421 PRVWRPRLPSPHPSLHNIPVPEETNYLGNTPMPFSSLPPTDESICKYITYNSTGIGICAYN 480
Qy      546 YMEIGTSSLLDSTNTNFKKEEPAKYQAI FDNNTSLDKHLDP IRENIGKHKNCARL 605
Db      481 YMEIGTSSLLDSTNTNFKKEEPAKYQAI FDNNTSLDKHLDP IRENIGKHKNCARL 540
Qy      606 GFTQSQIDEIDHDYERDGLKEKYOMLQKWMREGIGATVGKLAQALHQC SRIDLSSL 665
Db      541 GFTQSQIDEIDHDYERDGLKEKYOMLQKWMREGIGATVGKLAQALHQC SRIDLSSL 600

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Qy      666 IYVSON 671
Db      601 IYVSON 606

RESULT 11
US-60-455-444-6357
; Sequence 6357, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01455
; CURRENT APPLICATION NUMBER: US/60/455,444
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6357
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-455-444-6357

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Query Match      90.4%; Score 3204; DB 7; Length 606;
Best Local Similarity 99.8%; Pred. No. 3.1e-247;
Matches 605; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      66 MMNRLRHSRVYKLLGVIIEEGKYSLVMEYMEKGNLMHVLKAKMSTPLSVKRIILEIEG 125
Db      1 MMNRLRHSRVYKLLGVIIEEGKYSLVMEYMEKGNLMHVLKAKMSTPLSVKRIILEIEG 60
Qy      126 MCVLHGKGVIRKDLKPENILVNDNFHRIADLGLASFWMKSKLNNEEHNEELREVDGTAKK 185
Db      61 MCVLHGKGVIRKDLKPENILVNDNFHRIADLGLASFWMKSKLNNEEHNEELREVDGTAKK 120
Qy      186 NGCTLYMAPHLNDVNAKPTKESDVYSFAVVLNAIFANKPEYENALICEOOLIMCISGN 245
Db      121 NGCTLYMAPHLNDVNAKPTKESDVYSFAVVLNAIFANKPEYENALICEOOLIMCISGN 180
Qy      246 RPDVDITEYCPRREIISLMKLCWEANPEARPTFGIEEKFPRFYLSQLEESVEEDVSKL 305
Db      181 RPDVDITEYCPRREIISLMKLCWEANPEARPTFGIEEKFPRFYLSQLEESVEEDVSKL 240
Qy      306 KEYSNENAVVRKMSQLODCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWFAPSLEH 365
Db      241 KEYSNENAVVRKMSQLODCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWFAPSLEH 300
Qy      366 POENEPBSLOKLODEANYHLXGSRMDROTQORONAVAYNREBERRRRVSHDFFAQR 425
Db      301 POENEPBSLOKLODEANYHLXGSRMDROTQORONAVAYNREBERRRRVSHDFFAQR 360
Qy      426 YENFONTEGKGTVYSSAASHGNAVHOPSGLTQPOVLYONNGLYSSHGFGTRPLDPTAG 485
Db      361 YENFONTEGKGTAVSSAASHGNAVHOPSGLTQPOVLYONNGLYSSHGFGTRPLDPTAG 420
Qy      486 PRVWRPRLPSPHPSLHNIPVPEETNYLGNTPMPFSSLPPTDESICKYITYNSTGIGICAYN 545
Db      421 PRVWRPRLPSPHPSLHNIPVPEETNYLGNTPMPFSSLPPTDESICKYITYNSTGIGICAYN 480
Qy      546 YMEIGTSSLLDSTNTNFKKEEPAKYQAI FDNNTSLDKHLDP IRENIGKHKNCARL 605
Db      481 YMEIGTSSLLDSTNTNFKKEEPAKYQAI FDNNTSLDKHLDP IRENIGKHKNCARL 540
Qy      606 GFTQSQIDEIDHDYERDGLKEKYOMLQKWMREGIGATVGKLAQALHQC SRIDLSSL 665
Db      541 GFTQSQIDEIDHDYERDGLKEKYOMLQKWMREGIGATVGKLAQALHQC SRIDLSSL 600

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RESULT 12
US-60-465-241-6357
: Sequence 6357, Application US/60465241
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: BEGOVICH, Ann
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001468
: CURRENT APPLICATION NUMBER: US/60/465, 241
: CURRENT FILING DATE: 2003-04-23
: NUMBER OF SEQ ID NOS: 258418
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6357
: LENGTH: 606
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-465-241-6357

Query Match          90.4%: Score 3204; DB 7; Length 606;
Best Local Similarity 99.8%: Pred. No. 3.1e-247;
Matches 605: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 MANNLRHSRVYKLLGVIIIEGKYSLYMEYMEKGNLMHVLAEMSTPLSVKGRILLIEIG 125
DB 1 MANNLRHSRVYKLLGVIIIEGKYSLYMEYMEKGNLMHVLAEMSTPLSVKGRILLIEIG 60
QY 126 MCYIHKGVYHKDLKPEYILVNDNFHIKIDGLASFVKMSKLNNEEHNEIREVDTAKK 185
DB 61 MCYIHKGVYHKDLKPEYILVNDNFHIKIDGLASFVKMSKLNNEEHNEIREVDTAKK 120
QY 186 NGGLTYMAPRHLNDVNAKPTKESDYVSAFVYLWAFIRKPEYENATECOOLIMCKISGN 245
DB 121 NGGLTYMAPRHLNDVNAKPTKESDYVSAFVYLWAFIRKPEYENATECOOLIMCKISGN 180
QY 246 RPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKFRFYLSOLEEVEEDVSKLK 305
DB 181 RPVDVDTTEYCPREIISLMKLCWEANPEARPTFGIEKFRFYLSOLEEVEEDVSKLK 240
QY 306 KEYSNENAVYKRMOSLDLCVAVPSSNSNATEQPGSLHSSOGIGMGVPEESWAPSLIEH 365
DB 241 KEYSNENAVYKRMOSLDLCVAVPSSNSNATEQPGSLHSSOGIGMGVPEESWAPSLIEH 300
QY 366 POENEPSSLOSKLDDENANYHLGSRMDROTQOORONAVYREERERRRVSHDPAOQRP 425
DB 301 POENEPSSLOSKLDDENANYHLGSRMDROTQOORONAVYREERERRRVSHDPAOQRP 360
QY 426 YENFQNTGKGTYSASAASHGNVAHOPSGLTSPQVLYQNNGLYSSHGFGTRPLDPGTAG 485
DB 361 YENFQNTGKGTYSASAASHGNVAHOPSGLTSPQVLYQNNGLYSSHGFGTRPLDPGTAG 420
QY 486 PRVYRIPRIPSHMPLAHNIPVETNYLGNTPTMPFSSLPPTDESIKYTYTNSGTQIGAYN 545
DB 421 PRVYRIPRIPSHMPLAHNIPVETNYLGNTPTMPFSSLPPTDESIKYTYTNSGTQIGAYN 480
QY 546 YMEIGTSSSLDSTNTNFKKEPAKYOALFDNTSTLTDKLDPIRENLGKHMKNCAKRL 605
DB 481 YMEIGTSSSLDSTNTNFKKEPAKYOALFDNTSTLTDKLDPIRENLGKHMKNCAKRL 540
QY 606 GFTQSOIDEIDHDYERDGLKEKYQOMLOKVMWREGIGATYGLKLAQALHQCSTRIDLSL 665
DB 541 GFTQSOIDEIDHDYERDGLKEKYQOMLOKVMWREGIGATYGLKLAQALHQCSTRIDLSL 600
QY 666 IYVSQN 671
DB 601 IYVSQN 606
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RESULT 13
US-09-724-676-69182
: Sequence 69182, Application US/09724676
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 69182
: LENGTH: 406
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-724-676-69182

Query Match          50.9%: Score 1803; DB 5; Length 406;
Best Local Similarity 100.0%: Pred. No. 1.6e-135;
Matches 337: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SATEQPGSLHSSOGIGMGVPEESWAPSLIEHPOENEPSSLOSKLDDENANYHLGSRMDRO 394
DB 70 SATEQPGSLHSSOGIGMGVPEESWAPSLIEHPOENEPSSLOSKLDDENANYHLGSRMDRO 129
QY 395 TKOOPRONAVYANREERERRRVSHDPAOQRPYENFQNTGKGTYSASAASHGNVAHOPSG 454
DB 130 TKOOPRONAVYANREERERRRVSHDPAOQRPYENFQNTGKGTYSASAASHGNVAHOPSG 189
QY 455 LTSQPOVLYQNNGLYSSHGFGTRPLDPGTAGRVYRIPRIPSHMPLAHNIPVETNYLGNT 514
DB 190 LTSQPOVLYQNNGLYSSHGFGTRPLDPGTAGRVYRIPRIPSHMPLAHNIPVETNYLGNT 249
QY 515 PTMPFSSLPPTDESIKYTYTNSGTQIGAYNVAETGSSSLDSTNTNFKKEPAKYOAL 574
DB 250 PTMPFSSLPPTDESIKYTYTNSGTQIGAYNVAETGSSSLDSTNTNFKKEPAKYOAL 309
QY 575 IFDNTTSLTDKHLDPIRENLGKHMKNCAKRLGFTQSOIDEIDHDYERDGLKEKYQOMLOK 634
DB 310 IFDNTTSLTDKHLDPIRENLGKHMKNCAKRLGFTQSOIDEIDHDYERDGLKEKYQOMLOK 369
QY 635 WVMREGIGATYGLKLAQALHQCSTRIDLSLIYVSQN 671
DB 370 WVMREGIGATYGLKLAQALHQCSTRIDLSLIYVSQN 406

RESULT 14
US-09-724-676a-69182
: Sequence 69182, Application US/09724676a
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676a
: CURRENT FILING DATE: 2000-11-28
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 69182
: LENGTH: 406
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-724-676a-69182

Query Match          50.9%: Score 1803; DB 5; Length 406;
Best Local Similarity 100.0%: Pred. No. 1.6e-135;
Matches 337: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 SATEQPGSLHSSOGIGMGVPEESWAPSLIEHPOENEPSSLOSKLDDENANYHLGSRMDRO 394
DB 70 SATEQPGSLHSSOGIGMGVPEESWAPSLIEHPOENEPSSLOSKLDDENANYHLGSRMDRO 129
QY 395 TKOOPRONAVYANREERERRRVSHDPAOQRPYENFQNTGKGTYSASAASHGNVAHOPSG 454
DB 130 TKOOPRONAVYANREERERRRVSHDPAOQRPYENFQNTGKGTYSASAASHGNVAHOPSG 189
QY 455 LTSQPOVLYQNNGLYSSHGFGTRPLDPGTAGRVYRIPRIPSHMPLAHNIPVETNYLGNT 514
DB 190 LTSQPOVLYQNNGLYSSHGFGTRPLDPGTAGRVYRIPRIPSHMPLAHNIPVETNYLGNT 249
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Db 190 LTSQPVLYXNNGLYSHGFGRPLDPTAGRWYRPIPSHMSLNIPVETNYLGNT 249
QY 515 PTMPFSSLPPTDESISIKYTIYNSTGIQIGAYNMEIGTSSSLDSTNTNFKKEEPAKYQA 574
Db 250 PTMPFSSLPPTDESISIKYTIYNSTGIQIGAYNMEIGTSSSLDSTNTNFKKEEPAKYQA 309
QY 575 IFDNTTSLTDKHLDPRENLGKHWKNCARKLGFTQSQIDETDHDYERDGLKEKYQMLQK 634
Db 310 IFDNTTSLTDKHLDPRENLGKHWKNCARKLGFTQSQIDETDHDYERDGLKEKYQMLQK 369
QY 635 WWMREGIKGATVYKLAQALHQCSTRIDLSSLIYVSQN 671
Db 370 WWMREGIKGATVYKLAQALHQCSTRIDLSSLIYVSQN 406
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RESULT 15
US-09-724-676-69183
; Sequence 69183, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69183
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-69183
```

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Query Match 29.8%; Score 1055; DB 5; Length 256;
Best Local Similarity 96.1%; Pred. No. 5, 1e-76;
Matches 197; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 467 GLYSSHGFGTRPLDPTAGRWYRPIPSHMSLNIPVETNYLGNTPTMPFSSLPPTD 526
Db 52 GYFIDSSVGTTRPLDPTAGRWYRPIPSHMSLNIPVETNYLGNTPTMPFSSLPPTD 111
QY 527 ESIKYTIYNSTGIQIGAYNMEIGTSSSLDSTNTNFKKEEPAKYQAI FDN TTS L TDKH 586
Db 112 ESIKYTIYNSTGIQIGAYNMEIGTSSSLDSTNTNFKKEEPAKYQAI FDN TTS L TDKH 171
QY 587 LDPITRENLGKHWKNCARKLGFTQSQIDETDHDYERDGLKEKYQMLQKWWMREGIKGATV 646
Db 172 LDPITRENLGKHWKNCARKLGFTQSQIDETDHDYERDGLKEKYQMLQKWWMREGIKGATV 231
QY 647 GKLAQALHQCSTRIDLSSLIYVSQN 671
Db 232 GKLAQALHQCSTRIDLSSLIYVSQN 256
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Search completed: June 21, 2003, 16:24:18
Job time : 115 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: June 25, 2003, 19:49:40 ; Search time 4006 Seconds
(without alignments)
4874.684 Million cell updates/sec

Title: US-09-981-397A-16
Perfect score: 3545
Sequence: 1 MOPDMSLIVIKMKSSDFLES.....ALHQCSTRDILSLIYVSON 671

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3545	100.0	2617	6	AX429238
3	3545	100.0	2617	6	AX460995
4	3545	100.0	2617	6	HSU50062
5	3529	99.5	2137	6	168123
6	3505	98.9	9687	6	AR165919
7	2423.5	68.4	2268	10	MMU25995
8	2423.5	68.4	2268	10	HSU25994
9	1971	55.6	1240	9	AK096523
10	1753.5	49.5	2862	9	AK096523
11	1040	29.3	149546	9	HS40816
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13	583.5	16.5	150691	2	AC131143
14	448	12.6	1873	6	AR105327
15	448	12.6	1873	6	AX067676
16	446	12.6	1557	6	AR105328
17	446	12.6	1557	6	AX067677
18	435	12.3	1557	6	AF156884
19	423.5	11.9	3876	9	AK027424
20	419.5	11.8	3879	9	HS4278016
21	414.5	11.7	3882	9	AB047783
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36	371	10.5	1898	9	BC004553
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39	371	10.5	1931	6	AR205634
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RESULT 1

ALIGNMENTS

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LOCUS ARI45196 2016 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6211337.
ACCESSION ARI45196
VERSION ARI45196.1 GI:15107063
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2016)
AUTHORS Baichwal, V.R., Huang, J., Hsu, H. and Goeddel, D.V.
TITLE RIP: novel human protein involved in tumor necrosis factor signal transduction
JOURNAL Patent: US 6211337-A 1 03-APR-2001;
FEATURES Location/Qualifiers
source 1..2016
BASE COUNT 629 a 446 c 514 g 427 t
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Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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QY 121 GluIleIleGlnGlnGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
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Db 1621 ATTGAGACCTTACATATTTATGAGATGTGTGCGACGAGTTCATCATCATACTAGACAGACA 1680
QY 561 AsnThrAsnPheLysGlnGlnProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
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Oy	581	serleuPrrAspLySHSLsLeuAspProllaArgLlUsaNsLeuGlyLysSHISrPLysAsn	600
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Oy	601	CysAlaIarqLySLsLeuGlyPheThGlnSerClnlIleAspGluIleAspPHISAspTyGlu	620
Db	1801	TGTGCCCCATAACCTGGGCTTCACACAGCTCAGATTGATGAATTTAGCCATGACTATAG	18600
Oy	621	ArgAspGlyLeuLySGluLysValTyGlnMetLeuGlnLysrTPValMetArgGluGly	640
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Oy	641	LlelySGlyAlaThrValGlyLysLeuAlaIleAlaIleuHISGlnCysSerArgIleAsp	660
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ACCESSION	AX429238		
VERSION	AX429238.1	GI:21540549	
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AUTHORS			
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Oy	61	LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly	80
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OY	401	GlnAsnValAlaTrpAsnArgGluGluGluLuhArgArgArgValSerHIsAspProPhe	420
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 LOCUS Definition Sequence 1 from Patent WO0236148.
 AX460995
 AX460995.1 GI:21726224
 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Tschoop, J. and Holler, N.
 TITLE Use of death receptor ligands or rip to initiate the
 non-caspase-dependent cell death and compounds for inhibition of
 the non-caspase-dependent cell death
 Patent: WO 0236148-A 1 10-MAY-2002;
 JOURNAL Apotech Research and Development Ltd. (CH)
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 REFERENCE 1 (bases 1 to 2617)
 Huang, J., Hsu, H., Baichwal, V. and Goeddel, D. V.
 TNF-dependent recruitment of the protein kinase RIP to the TNF
 receptor-1 signaling complex
 Immunity 4 (4), 387-396 (1996)
 JOURNAL MEDLINE 96200892
 PUBMED 8612133
 REFERENCE 2 (bases 1 to 2617)
 Huang, J., Hsu, H., Baichwal, V. R. and Goeddel, D. V.
 Direct Submission
 Submitted (26-FEB-1996) Biology, Tularik Inc., 270 East Grand
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 JOURNAL 3 (bases 1 to 2617)
 Huang, J., Hsu, H., Baichwal, V. R. and Goeddel, D. V.
 Direct Submission
 Submitted (18-AUG-1998) Biology, Tularik Inc., 270 East Grand
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 JOURNAL 1 (bases 1 to 2617)
 Sequence update by submitter
 On Aug 18, 1998 this sequence version replaced gi:1236942.
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 AUTHORS Leder, P., Seed, B., Stanger, B. Z., Lee, T.-H. and Kim, E.
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Db	1921	ATTAAGGAGCGACAGGTGGGAGCACTGGCCACGCGCTCCACAGATGTTCACAGATGCAC			1980
Qy	661	LeuLeuSerSerLeuIleTyrValSerGlnAsn			671
Db	1981	CTTCTGAGCACGCTTGATTTACGTACGACGACGAC			2013

RESULT 6

LOCUS	AR165919				
DEFINITION	Sequence 2 from patent US 6280937.	DNA	linear	PAT 17-OCT-2001	
ACCESSION	AR165919				
VERSION	AR165919.1	GI:16241007			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 9687)				
AUTHORS	Imo,Y., Yu,P.,Men. and Lorens,J.				
TITLE	Shuttle vectors				
JOURNAL	Patent: US 6280937-A 2 28-AUG-2001;				
FEATURES	Location/Qualifiers				
source	1..9687				

BASE COUNT	2643 a	2220 c	2370 g	2454 t
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Score:	3505.00	Matches: 668		
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Query Match:	98.87%	Indels: 1		
DB:	6	Gaps: 0		

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QY	22	GluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisAspGlyThrGlnGlyLeu	41
Db	1194	GAACTGGACAGCGGAGGCTTTGGGAAGGTGCTGTGTGTTTCCACAAACCCAGGAGACT	1253
QY	42	MetIleMetLysThrValTyrLysGlyProAsnGlyIleGlnHisAsnGluAlaLeuLeu	61
Db	1254	ATGATCATGAAAAACAGTGTACAAAGGGGCCCAATGCATGTGGACAAACGAGGCCCTGTG	1313
QY	62	GluGlnAlaLeuysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGlyVal	81
Db	1314	GAGAGGCGGAAGATGATGATGACAGACTGAGACACAGCCGGGTCGTGAAGCTCTTGGCGCT	1373
QY	82	IleIleGlnGlnGlyLysTyrSerLeuValMetClnIlyrMetGlnLysGlyAsnLeuMet	101
Db	1374	ATCTATAAAGGAAGGAAGTACTCCCTGCTGATGAGATCAATGGAGAAGGGCAACTGATG	1433
QY	102	HisValLeuysAlaGlnMetSerThrProLeuSerValLysGlyArgIleIleLeuGln	121
Db	1434	CACGTGCTGAAGCGGAGATGAGTACCTCCGTTTCTGTAAAGAGAAAGATATTTTGGGAA	1493
QY	122	IleIleGlnGlnMetCysTyrGluLeuHisGlyLysGlyValAlaIleHisLysAspLeuLysPro	141

Dd	1494	ATCATTTGAGGAATAGTCTACTCTTACATACGA - AAAGGGCTGTATACAAAGGACCTGGAAGCCT	1552
Oy	142	GLuSnIleuEnuAlaSpaSnAPPhEhISIlEluSIlleAlaSpIeuGIuLeuAlaSer	161
Dd	1553	GAAATATTCCTGTGTGTAATAGTACTTCCACATTTAAGATGCGAGACCTCGGGCTTGGCTCC	1612
Oy	162	PhelSheTrPSeRtYsLeuASnSnGIuGhISnGIuLeuARgIuValASpGIy	181
Dd	1613	TTTAAGATGTGGACCAACTGCATTAATTAAGAGAGCACACATGAGCTGAGCGCAAGTCGACGGC	1672
Oy	182	ThrlAlaYsIySAnGIlYgIYThlEuTYTYTYMeAlAPrOGIuHISleuSnAPvAl	201
Dd	1673	ACCCTTAAGAAAGATGGCGCACCCCTCTACTCATGCGGCCGACGACCTGTAATGACGTC	1732
Oy	202	ASnAlaYsPrOThrGIuLYsSerASpValATTYSerPheAlaValLeuTrpAlaIle	221
Dd	1733	AACGCAAAAGCCACAGAGAAAGTGGATGTACAGCTTTTGCTATGACTCTGGCGGATTA	1792
Oy	222	PheAlaSnIySGIuPrOTrYrGIuASnAlaIlEcySgIuGInGInLeuIlEmeCYsIlE	241
Dd	1793	TTTGCAATATAGAGAGCCATMTGAAATAGCTATCTGTGAGAGCAGTGTGATTAATGTGCATA	1852
Oy	242	LYsSerGIyASnARgPrOASpValASpASpIlEThrGIuTYrCYsPrOARgIuIlElle	261
Dd	1853	AAATCTGGGAACAGGCGATGTGCGATGCATGCAGTACGACGACCCCAAGAAATATTC	1912
Oy	262	SeRleuMeTrISeuCYsTrPrGIuAlaASnPrOGIuAlaARgPrOThrPhePrOGIyIlE	281
Dd	1913	AGTCTCATGANGCTCTCTCTGGAGGCGCAATCTCGGAAGCTGGCGGACATTTCTGTGCATT	1972
Oy	282	GIuGIuLYsPheARgPrOPheTYrLeuSerGIuLeuGIuSerValGIuIuSnAPvAl	301
Dd	1973	GAAACAAAATTTAGCCCTTTTATTATTAAGCATTTAGAAAGAAAGTGTAGAAAGAGACGIG	2032
Oy	302	LYsSerLeuYsIySGIuTYrSerASnGIuASnAlaValLYsARgMeGIuSerIeu	321
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Oy	322	GIuIeuASpCYsValAlaValPrOSeRSeRfISerASnSerIaThrGIuGInPrOGIy	341
Dd	2093	CAACTTATATTGTGGGAGTACCTTCAAGCCGGTCAAAATTCACCCACAAACAGCCGTGT	2152
Oy	342	SeRleuHISerSeRGIuGIuLeuGIuMeGIuPrOValGIuIuSerTrpPheAlaPrO	361
Dd	2153	TCACTGCACAGTTCOCAGGGACTTGGATGGTCGTCGTGAGAGAGTCGTGGTTGCTCCT	2212
Oy	362	SeRleuGIuHISPrOGIuGIuIuASnGIuPrOSeRleuGInSerLYsIeuGIuASpGIu	381
Dd	2213	TCCCTGGAGACCCACAGAAAGAAATGAGCCGACGCTGACAGTAAATCCACAGCAGNA	2272
Oy	382	AlaASpTYrHISleuTYrGIySerARgMeLAsPARGInThrLYsInGInPrOARgIn	401
Dd	2273	GCCAACTTACCATCTTTATGCGACCCCGATGGAACAGGACAGCGAAMACAGAGCCCAACAG	2332
Oy	402	ASnValAlaTYrASnARgGIuGIuIuARgARgARgARgValSerfISASpPrOpheAla	421
Dd	2333	AATGTGGCTTACAAACAGAGAGAGAAAGGACGAGGCTCTCCATGACCTTTTGCA	2392
Oy	422	GIuGIuNARgPrOTrYrGIuASnPrOGInASnThrGIuGIuLYsGIuThrValTYrSerSer	441
Dd	2393	CAGCAAAAGACCTTACAGGAATTTTTCAGAAATACAGAGGAAAGGCACTGTTATTCCAGT	2452
Oy	442	AlaAlaSerHISGIyASnAlaValHISGInPrOSeRGIyLeuThSerGIuPrOGInVal	461
Dd	2453	GCACCCAGTATGGTAATGACAGTGACACACCCCTCGAGGGCTCACCCGCAACCTCAAGTA	2512
Oy	462	LeuTYrGIuASnASnGIuLeuTYrSerSerHISGIuPheGIuThrARgPrOleuASpPrO	481
Dd	2513	CTGTATGACAAATGATGATTATATAGCTCAGACGGCTTTGGAAAGAACACCTGATGCA	2572
Oy	482	GIuThrAlaGIuPrOARgValTrpTYrARgPrOlePrOSeRHisMePrOSeRleuHIS	501

OY	302	LysSerLeuMySLysSLyUTYrSerASnGLuaSnAlaValValLysArgMetGlnSerLeu	321
Db	2033	AAGAGTTTAAAGAAGAGTATTCATAACGAAAGAGAGTGTGAAGGAATGCAAGTCCTCT	2092
OY	322	GlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnProGly	341
Db	2093	CAACTTGATGTGTGGCAGTACTTCAGAGCGGTTCAAATTTCAGCCACACACAGCTGGT	2152
OY	342	SerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGlnuSerTrpPheAlaPro	361
Db	2153	TCACCTGCACAGTCCCGAGGACTGGGATGGTCCTGGAGAGAGCTCGTGGCTCCT	2212
OY	362	SerLeuGlnHisProGlnGlnGluAsnGlnProSerLeuGlnSerLysLeuGlnAspGlu	381
Db	2213	TCCCTGGAGCACCCACAGAAGAGMATGAGCCACGCTGCAGAGTAAATCCANAGACANA	2272
OY	382	AlaAsnTrpHisLeuTrpGlySerArgMetAspArgGlnThrLysGlnInProArgGln	401
Db	2273	GCCAACTACCAATCTTTATGCGACGCCGATGACAGGACAGCAGAAACAGCAGCCACAGACAG	2332
OY	402	AsnValAlaIarYrrAsnArgGluGlnGluArgArgArgArgValSerHisAspProPheAla	421
Db	2333	AATGTGCTTACAAACAGAGAGGAGAAAGGACGACGAGGCTCCCATATCCCTTTTGCA	2392
OY	422	GlnGlnArgProTrpGluAsnProGlnAsnThrGlnGlyLysGlyThrValTrpSerSer	441
Db	2393	CAGCAAGACCTTACAGAGAAATTTTCAAGAAATACAGAGAGGAAAGGCACTGTTATTCACAT	2452
OY	442	AlaAlaSerHisGlyAsnAlaValAlaHisGlnProSerGlyLeuThrSerGlnProGlnVal	461
Db	2453	GCACCCAGTATGTTAATGCAGTGCACACCCCTTCAGGGGCTCACCGCCACACCTCAAGTA	2512
OY	462	LeuTrpGlnAsnAsnGlyLeuTrpSerSerHisGlyPheGlyThrThrArgProLeuAspPro	481
Db	2513	CTGATATGACAAATGATATATATAGCTCACATGGCTTTGGACAAAGACCACTGCATCCA	2572
OY	482	GlyThrAlaGlyProArgValTrpTrpArgProIleProSerHisMetProSerLeuHis	501

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 Oy 522 LeuProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIle 541
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 LOCUS Sequence 14 from patent US 5674734.
 DEFINITION 168122
 ACCESSION 168122.1 GI:2830244
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 KEYWORDS
 SOURCE
 ORGANISM
 Unknwn.
 Unclassified.
 REFERENCE
 1 (bases 1 to 2268)
 AUTHORS Leder, P., Seed, B., Stanger, B. Z., Lee, T. -H. and Kim, E.
 TITLE Cell death protein
 JOURNAL Patent: US 5674734-A 14 07-OCT-1997;
 FEATURES
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 Best local Similarity: 69.79% Mismatches: 116
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 Oy 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyCysPheHisArgThrGlnGly 40

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 Oy 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
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LOCUS
DEFINITION Mus musculus cell death protein (RIP) mRNA, complete cds.
ACCESSION U25995.1 GI:829618
VERSION U25995.1 GI:829618
KEYWORDS Fas; TNF receptor.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2268)
AUTHORS Stanger,B.Z., Leder,P., Lee,T.H., Kim,E. and Seed,B.
TITLE RIP: a novel protein containing a death domain that interacts with
Fas/Apo-1 (CD95) in yeast and causes cell death

REFERENCE
1 (bases 1 to 2268)
AUTHORS Stanger,B.Z., Leder,P., Lee,T.H., Kim,E. and Seed,B.
TITLE RIP: a novel protein containing a death domain that interacts with
Fas/Apo-1 (CD95) in yeast and causes cell death

JOURNAL Cell 81 (4), 513-523 (1995)
MEDLINE 95277838
PUBMED 7538908
REFERENCE 2 (bases 1 to 2268)
AUTHORS Stanger,B.Z.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-1995) Ben Z. Stanger, Genetics, Harvard Medical
School, 200 Longwood Avenue, Boston, MA 02115, USA
FEATURES
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Percent Similarity: 80.21% Conservative: 70
Best Local Similarity: 69.79% Mismatches: 116
Query Match: 68.36% Indels: 17
DB: 10 Gaps: 5
US-09-981-397A-16 (1-671) x MMU25995 (1-2268)

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Oy		520	SerSerLeuProProThrAspGluSerIleLysTrpThrIleTryAsnSerThrGlyIle	539
Dd		1576	TTCCTCTGGGCCAGTAGACAGATGACATCTCATTAATAATATCTATATTCATATAGTTCGGTAT	1635
Oy		540	GlnIleGlyAlaTryAsnTrpMetGluIleGlyGlyThrSerSerSerLeuAspSer	559
Dd		1636	CAGATTGGAAACCAACATTTATATGATGTTGGACTGATTCAC-----CAACCA	1683
Oy		560	ThrSnrnThrAsnPheLysGluGluProAlaAlaLysTrpGlnAlaIlePheAspAsnThr	579
Dd		1684	CCAACCAACTACTTSCAAAAGAGAGTGCACCTTCAGACACCAAGGCATCTTGGATTAACACC	1743
Oy		580	ThrSerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTrpLys	599
Dd		1744	ACTAGTCTGACTGATGAACACCTTAACCTCTTCAGGGAAACCTGGGAAGGCACTGGGAAA	1803
Oy		600	AsnCysAlaArgLysLeuGlyPheTrcGlnSerGlnIleAspGluIleAspHisAspTrp	619
Dd		1804	AACGTGCCCCCAAGCTGCGCTTCACGTACAGTCAGATCGATGAATCGAACCAAGACATAT	1863
Oy		620	GluArgAspGlyLeuLysGluLysValTyroIimelleuGlnLysTrpValMetArgGlu	639
Dd		1864	GAAAGAGATGACATCGAAAGAGAAAGATTACCAAATGCTTCGAAAGTGGCTGATCCGGGA	1923
Oy		640	GlyIleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIle	659
Dd		1924	GGCACCAAAAGGGGCCACAGTGGGAAAGTGGCCCAAGGACCTTCACCAATGTTGCAGAGTA	1983
Oy		660	AspLeuSerSerSerLeuIleTryValSerGlnAsn	671
Dd		1984	GACCTGCTGAAACCACTTGATTCGTGCCACGACAGAC	2019
RESULT 9				
LOCUS	HSU25994	1240 bp	mRNA	linear PRI 24-MAY-1995
DEFINITION	Human cell death protein (RIP) mRNA, partial cds.			
ACCESSION	U25994			
VERSION	U25994.1	GI:829616		
KEYWORDS	Fas; TNF receptor.			
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE				
AUTHORS	Stanger,B.Z., Leder,P., Lee,T.H., Kim,E. and Seed,B.			
TITLE	RIP: a novel protein containing a death domain that interacts with			
	Fas/Apo-1 (CD95) in yeast and causes cell death			
JOURNAL	Cell 81 (4), 513-523 (1995)			
MEDLINE	95377838			
PUBMED	7538908			
REFERENCE	2 (bases 1 to 1240)			
AUTHORS	Stanger,B.Z.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-MAY-1995) Ben Z. Stanger, Genetics, Harvard Medical			
	School, 200 Longwood Avenue, Boston, MA 02115, USA			
FEATURES				
source	1..1240			


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1..1240
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/db_xref="GI:829617"
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QVLYQNGLYSSHGFGTRPDPGAPGRVWRPISPMPSLNIPVETNYLGSPTM
PFSLPPTDESIXKTYINSTGIGIAGVNYMEIGTSSLDSTNINKEEPAKYQAI
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BASE COUNT 380 a 295 c 303 g 262 t

ORIGIN

Alignment Scores:

Pred. No.:	5.88e-126	Length:	1240
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Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.73%	Mismatches:	0
Query Match:	55.60%	Indels:	0
DB:	9	Gaps:	0

US-09-981-397a-16 (1-671) x HSU25994 (1-1240)

QY 300 AspValysSerLeuLysGlyTyrSerAsnGluAsnAlaValLysArgMetGln 319

DB 1 GACCTGAAGATTAAAGAAAGAGTATTCAACGAAATGCACTGTGAAGAGAAATGCAG 60

QY 320 SerLeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGln 339

DB 61 TCTCTTAACCTGATGTGTGGGAGTACCTTCAAGCCGCTCAATTCAGCCACGAAACAG 120

QY 340 ProGlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluLysTrpPhe 359

DB 121 CCTGTGTCACCTGCACAGATCCAGGAGCTGGAGTGGGTCTGTGAGAGAGTCTGTGTT 180

QY 360 AlaProSerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGln 379

DB 181 GCTCTCTTCCCTGGGACCCACAGAAAGAGATAGCCCGCTGCAGAGTAAACTCCAA 240

QY 380 AspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnPro 399

DB 241 GACCAACCCCACTTCCATCTTTATGCGACCGCATGGACAGGACGAGCAACAGCAGCC 300

QY 400 ArgGlnAsnValAlaTyrAsnArgGluGluArgArgArgValSerHisAspPro 419

DB 301 AGACAGAAATGGCTTACACAGAGAGAGAGAAAGAGAGAGAGAGGCTCCCATGACCT 360

QY 420 PheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyr 439

DB 361 TTTGCAAGCAAGAACCTTTCAGCAATTTTCAGAAATTCAGAGGAAAGCACACTTTAT 420

QY 440 SerSerAlaAsnSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnPro 459

DB 421 TTCAGTGCACCACTGATGTGAAGCGATGCGACCGCATCAGGGCTCACCAGCCACCT 480

QY 460 GlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeu 479

DB 481 CAAGTACTGATCAGAACATGATATATAGCTCACATGGCTTGGAAACAAGCAGCTG 540

QY 480 AspProGlyThrAlaGlyProAlaGlyValTyrTyrArgProIleProSerHisMetProSer 499

DB 541 GATTCACAGAACACAGGTCCAGAGTTGGTACAGGCGCAATTCCAAGTCAATATGCTAGT 600

QY 500 LeuHisAsnIleProValProGluThrAsnTyrLeuGlnLysAsnThrProIleMetProPhe 519

DB 601 CTGCATATATCCAGTCCCTGAGACCAACTATCTAGAAAATCTCCACCACATCCATTC 660

QY 520 SerSerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyTle 539

DB 661 AGCTCTTGGCCACCAACAGATGATCTATATAATATACCATATACATAGTACTGGCAT 720

QY 540 GlnIleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerLeuLeuAspSer 559

DB 721 CAGATTGAGAGCTCAATTTATGAGATTGGTGGAGGAGGATTGATCATCAGTACAGACG 780

QY 560 ThrAsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAspThr 579

DB 781 ACAATATGCAACTTCAAGAGACCCAGCTGCTAAGTACCAAGCTATCTTGTATTAAC 840

QY 580 ThrSerLeuThrAspLysHisLeuAspProIleArgLysLysLeuGlyLysHisTrpLys 599

DB 841 ACTAGTGTGACGAGTAAACACCTGACCCATCGAGGAAATCTGGGAAAGCAGCTGAAA 900

QY 600 AsnCysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyr 619

DB 901 AACTGTCCCGTAAACTGGGCTTCACACAGTCTCATGATGATGAATTCACCATGACTAT 960

QY 620 GlnArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTrpValMetArgGlu 639

DB 961 GAGCGAGATGAGCTGAAAGAAAGAGTTTACCAGATGCTCCAAAAGTGGCGATGAGGAA 1020

QY 640 GlyIleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIle 659

DB 1021 GGCAATAAGGAGAGCCAGCTGGGAGAGCTGGCCAGGCGCTCCACAGTGTCCAGGATC 1080

QY 660 AspleuLeuSerSerLeuIleTyrValSerGlnAsn 671

DB 1081 GACCTCTGACAGAGCTGATTTACGTGACGACAGAC 1116

RESULT 10

AK096523

LOCUS

DEFINITION

AK096523 Homo sapiens cDNA FLJ39204 f1s, clone OCBF2005476, highly similar to SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-).

ACCESSION

AK096523

VERSION

AK096523.1 GI:21756039

KEYWORDS

oligo capping; f1s (full insert sequence).

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Magatsuna,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahara,K., Masuno,Y., Nagai,K. and Isogai,T.,

TITLE

NEDO human cDNA sequencing project

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 2862)

AUTHORS

Isogai,T. and Yamamoto,J.

TITLE

Direct Submission

JOURNAL

Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

Location/Qualifiers


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1. .2862
/organism="Homo sapiens"
/db.xref="taxon.9606"
/clone="OCB2005476"
/clone_type="brain"
/clone_id="OCB2005476"
/dev_stage="fetal"
/note="Cloning vector: PME18SFL3"

BASE COUNT      797 a      669 c      699 g      697 t
ORIGIN

Alignment Scores:
Pred. No.:      1,31e-110      Length:      2862
Score:          1753.50      Matches:      337
Percent Similarity: 91.83%      Conservative: 0
Best Local Similarity: 91.83%      Mismatches: 0
Query Match:      9      Indels:      30
                        Caps:      1

US-09-981-397A-16 (1-671) x AK096523 (1-2862)

OY      306  LysGluIyrSerAsnGluAsnAlaValAlLysArgMetGlnSerLeuGlnLeuAspCys 325
        |||||||
        2  AAAGAGATTCTCAAGAAATGCAAGTGTGAAGAGATGCAGTCTTCAACTGATGATGT 61

OY      326  ValAlaValAlProSerSerArgSerAsnSerAlaThrGluGlnProGlySerLeuHisSer 345
        |||||||
        62  GTGGCAGTACCTTAAGCGCGGTCAAAATTCACCCAGAACAGCCCTGGTTCACCTCAGCAGT 121

OY      346  SerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaProSerLeuGluHis 365
        |||||||
        122  TCCAGGAGACTGTGGATGGGTCTGTGAGAGAGTCTGGTGTGCTCCCTCCCTGGAGAGC 181

OY      366  ProGlnGluGluAsnGluProSerLeuGlnSerLeuGlnAspGluAlaAsnTyrHis 385
        |||||||
        182  CCACAAAGAGATGAGGCCAGCCAGCTCAGAGTAACTCCAAAGACCAAGCCACTACCAT 241

OY      386  LeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyr 405
        |||||||
        242  CTTTATGGCAGCCCATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 301

OY      406  AsnArgGluGluGluArgArgArgValSerHisAspProPheAla-GlnGlnArgPr 425
        |||||||
        302  AACGAGAGAGGAGAAAGAGAGCAGCAGGCTCCCATGACCTTTTGGACAGC----- 353

OY      425  CTrGlnAsnPhelGlnAsnThrGlnGlyLysGlyThrValTyrSerSerAlaAlaSerHi 445
        |||||||
        353  ----- 353

OY      445  sGlyAsnAlaValAlHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAs 465
        |||||||
        354  -----CCCTAGAGGCTCACCAGCCCAACCTCAAGTACTGATCAGAA 394

OY      465  nasGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaG 485
        |||||||
        395  CAATGGATTATATAGTCACTACGCTTGGAAACAAGCACTGATGCAGAACAGCAGG 454

OY      485  yProArgValTrpArgProIleProSerHisMetProSerLeuHisAsnIleProVa 505
        |||||||
        455  TCCAGAGTTTGGTACAGGCCCAATTCCAAGCATATGCTGATGATAATATATCCAGT 514

OY      505  lProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuProProTh 525
        |||||||
        515  GCCGAGACCAACACTATAGCAATATACACCACCATGCCATTCAGCTCCTGCCACACAC 574

OY      525  rAspGluSerIleLeuTyrThrIleTyrAsnSerThrGlyIleGlnIleGlyAlaTyrAs 545
        |||||||
        575  AGATGATCTATAATAATATACATATACAAATAGTACGATTCAGATTTGAGGCTCAAA 634

OY      545  nTyrMetGluIleGlyThrSerSerSerLeuLeuAspSerThrTrpAsnPhely 565
        |||||||
        635  TTATATGAGAGATTGGTGGAGAGAGTTCATCTACTAGACAGCAGCAATAATAGCAACTCA 694

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OY      565  sGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSerLeuThrAspLy 585
        |||||||
        695  AGAAGAGCCAGCTGCTAAGTACCAAGCTATTTGATATATACCACTACTGACAGCATAA 754

OY      585  sHisLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsnCysAlaArgLysLe 605
        |||||||
        755  ACACCTGGACCCATTCAGGAGAAATTCGCGAAGACACTGAGAAATATGTCCTTAACCT 814

OY      605  uGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGluArgAspGlyLeuLy 625
        |||||||
        815  GGGCTTCACACAGTCTCAGATTGATGAATTTGACCATGATCATATGAGCGAGATGCATGA 874

OY      625  sGluLysValTyrGlnMetLeuGlnLysTyrProValMetArgGluGlyIleLysGlyAlaTh 645
        |||||||
        875  AGAAAGGTTTACAGATGCTCCAAAGTGGGTATGAGGAGAGCATAAAGGAGCCAC 934

OY      645  rValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgTyrIleAspLeuSerSerLe 665
        |||||||
        935  GGTGGGAGAGCTGGCCAGCGGCTCCACCACTGTTTCCAGATGCACCTTTCAGACAGCTT 994

OY      665  uIleTyrValSerGlnAsn 671
        |||||||
        995  GATTTACGTACGCCAGAAC 1013

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RESULT 11
LOCUS      HS40E16      149546 bp      DNA      linear      PRI 10-MAR-2001
DEFINITION Human DNA sequence from clone RPI-40E16 on chromosome 6p24.1-25.3,
ACCESSION AL031963
VERSION    AL031963.40 GI:13235084
KEYWORDS   HTG.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
            1 (bases 1 to 149546)
REFERENCE  1
  AUTHORS  Sycamore,N.
  TITLE    Direct Submission
  JOURNAL  Submitted (02-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
            requests: clonerequests@sanger.ac.uk
            On Mar 5, 2001 this sequence version replaced gi:13235084.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TrEMBL; Wp:, WormPep; information on the WormPep
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep
            This sequence was generated from part of bacterial clone contigs of human
            chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
            Group. Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr6
            RPI-40E16 is from the library RPI-1 constructed by the group of
            Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pCYPAC2
            This sequence is the entire insert of clone RPI-40E16 The true left
            end of clone RPI-1112K15 is at 88226 in this sequence. The true
            right end of clone RPI-90J20 is at 9716 in this sequence.
            Location/Qualifiers

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FEATURES

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consensus"
1192. .1244
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consensus"
1245. .1465
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/note="L1P4 repeat: matches 5925. .6146 of consensus"
1466. .1868
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consensus"
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2319. .3009
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3010. .3306
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/note="AluY repeat: matches 3. .309 of consensus"
3307. .3358
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/note="MER4-internal repeat: matches 6204. .6255 of
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4056. .4303
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consensus"
4307. .4670
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4671. .4970
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/note="MER83 repeat: matches 389. .448 of consensus"
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17029. .17081
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/evidence=not_experimental
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32839. .33119
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35472. .35579
repeat_region
/note="3 copies 36 mer 76% conserved"
35488. .35577
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35581. .35638
repeat_region
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35653. .35710
repeat_region
/note="29 copies 2 mer ta 75% conserved"
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repeat_region
/note="WIR repeat: matches 21. .192 of consensus"
36485. .36963
repeat_region
/note="L1M2 repeat: matches 5603. .6111 of consensus"
37058. .37373
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repeat_region      38781. 38092
/noise="Alu0 repeat: matches 2. .301 of consensus"
repeat_region      39094. 39319
/noise="13 copies 2 mer at 100% conserved"
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Alignment Scores:

Pred. No.	1.44e-59	length:	119546
Score:	1040.00	Matches:	157
Percent Similarity:	92.00%	Conservative:	10
Best Local Similarity:	87.56%	Mismatches:	11
Query Match:	29.34%	Indels:	7
DB:	9	Gaps:	2

US-09-981-397A-16 (1-671) x HS40E16 (1-149546)

335 SerAlaThrGlnProGlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProVal 354

Db 6/872 TCAGCCACAGACAGCCCTGGTTCACCTGCACAGTTCGCCAGGACTTGGGATGGTCCCTGTG 67931

333 61UGUuser11pneadI0serLeuG1amISProGInG1uG1uashG1UProserLeu 3/4

[illegible][illegible]

Ov 395 ThrlVscG]nG]nProbaorcG]naenYaJAJatTvrdenAorc]oC]uDrncDrcDrcDrc A14

Db 68052 ACGAAACAGCAGCCAGACAGAATGTGGCTTACAACAGAGAGGAGGAAGGAGACCGAGG 68111

415 ValSerHisAspProPheAlaGlnIleArgProTyrGluAsnPheGlnAsnThrGluGly 434

Db 68112 GTCTCCATGACCCCTTTGCACAGCAAGACCTTACGAGAATTTTCAGAATACAGAGGA 68171

QY 435 LysGlyThrValTyrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGly 454

Db 68172 AAAGGCACTGCTTATTCCAGTGCAGCCAGTCATGGTAATGCAGTGCACCCAGCCCTCAGGG 68231

455 LeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPhe 474

Db 68232 CTTACCCAGCCCAACCTCAAGTACTGTATTCAGAACAAATGGATTATATAGCTCACATGGCTTT 68291

47 475 gylmuaigfrlobuasprloigymmaaaigylpfoaigvaliiipyiaigprollepio 494
|||||

U.S. DEPARTMENT OF AGRICULTURE
BUREAU OF PLANT INDUSTRY
WASHINGTON, D. C.

[illegible]

515 ProThrMetProPheSerSerLeuProProThraSc[usSer]alveturThrt]etvr 534

Db 68412 CCCACCATGCCATTCAGCTCCTTGCCACCAACAGGTAA-----TGGGCTCTTC 68459

QY 535 AsnSer-ThrGlyIleGlnIleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSe 554.

Db 68460 GATAGTCACAGCTTGTCTTT-----TTTATTTTTCAGAAATACAGCAACCAAGCAG 68513

QY	554	rSerLeuLeuAsp	558
----	-----	---------------	-----

Db 68514 CTCCTATTATAGAT 68526

RESULT 12
AC120978/C

LOCUS	AC120976	109832 bp	DNA	linear	HTG 23-JUL-2002
DEFINITION	Rattus norvegicus clone CH230-515P13, *** SEQUENCING IN PROGRESS				

RESULT	12				
AC120978/c					
LOCUS	AC120978	109832 bp	DNA	linear	HTG 23-Jul-2002
DEFINITION	Rattus norvegicus clone CH30-51SP13,***			SEQUENCING IN PROGRESS	
ACCESSION	AC120978				
VERSION	AC120978.3	GI:21902873			

KEYWORDS
SOURCE
ORGANIS

REFERENCE
AUTHORS

HTG: HTGS_PHASE1.
Rattus norvegicus.
Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 109832)

AUTHORS

Muzny,D.B., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amarantunga,H.C., Are,J.A., Ayalew,M., Banks,T., Barberia,J., Benton,J., Bimake,K., Blankenburg,K., Bonnah,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunhay,C., Birch,P., Burkelt,C., Burrell,K.L., Byrd,N.C., Carton,T.F., Carter,M., Cavazos,S.R., Chacko,U., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Day-Carroll,L., Deedrich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhardt,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsl,F., Howard,S., Huber,J., Hulyk,S., Humm,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovac,C., Kratochic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.I., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Lonsleged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Messer,E., Mawney,E., Mcleod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nokenkho,S., Oguh,M., Okunodu,G., Oraguine,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., PETERS,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savary,G., Scherger,S., Scott,G., Shen,H., Shoohtarl,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tameitisa,A., Tameits,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Teitford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wlaczek,R., Woodden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G., and Gibbs,R.

TITLE
Journal
Reference
Title
Journal

REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Unpublished
2 (bases 1 to 109832)
Morley,K.C.
Direct Submission
Submitted (14-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 109832)
Morley,K.C.
Direct Submission
Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 18, 2002 this sequence version replaced q1:21039617.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: GXXK
Center clone name: CH230-515P13
----- Summary Statistics -----
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye 100% of reads


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OY 435 LyseGlyThValYrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGly 454
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 107878 AAAGTCTTCTTCTTATCCACACACACACACACACACACACACACACACACAGG 107819
OY 455 LeuThSerGlnProGlnValLeuThyGlnAsnAsnGlyLeuThySerSerHisGlyPhe 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 107818 CCAAGCCAGCCAAATCAAGAGCCACCTTGGACACACAGAGATATATATCATCATGAGGTTT 107759
OY 475 GlyThArgProLeuAspProGlyThAlaGlyProAlaValThyArgProIlePro 494
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Db 107758 -----GGAGCTACAGAGTACAGAGATTTGTTATGGCCACAGCTA 107720
OY 495 SerHisMetProSerLeuHisAsnIleProValProGlyThAsnThyLeuGlyAsnThr 514
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Db 107719 AGCCATCATATATATGCTTATATAAACTGCTGCTGAGACACACATACACGACGATA 107660
OY 515 ProThMetProPheSerSerLeuProPro 524
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Db 107659 CCCACATGCATACATCTCTTGGACACA 107630

RESULT 13
AC131143/c 150691 bp DNA linear HTG 17-AUG-2002
LOCUS Rattus norvegicus clone CH230-76E20, *** SEQUENCING IN PROGRESS
DEFINITION *** 75 unordered pieces.
AC131143
AC131143.1 GI:22296630
VERSION HTG: HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 150691)
Muzny,D.,Marie., Metzker,M.,Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Ayalabecheh,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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Bernaldo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Centler,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
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Devilla,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
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Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
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Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hayes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M.,
Hollins,B., Howells,S., Huliy,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Jarkpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lepow,H., Leyvan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensonuwa,L., Louisedge,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindaratne,M., Mahmood,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A.,
Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
Morris,S., Munidas,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,
Newton,N., Nguyen,N., Norris,S., Nwakoeleneh,O., Okwoulu,H.,
Olariunsaogoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
Perez,A., Perez,L., Pfankoch,C., Plopper,F., Polindexter,A.,
Popovic,D., Primus,E., Pu,L.-L., Puzo,M., Quiroz,J., Rechlin,E.,
Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojs,A.,
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,
Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,
Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,
Svatek,A., Tabors,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
Tingey,A., Trejos,Z., Usmari,K., Valas,R., Vera,V., Villanara,D.,
Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R.,
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 150691)
Rat Genome Sequencing Consortium.
Submitted (17-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GNUV
Center clone name: CH230-76E20
----- Summary Statistics
Sequencing vector: plasmid;
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 81272 bases at least Q40
Consensus quality: 88571 bases at least Q30
Consensus quality: 93815 bases at least Q20
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank.draft.data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1192: contig of 1192 bp in length
1193 1292: gap of unknown length
1293 2321: contig of 1029 bp in length
2321 2421: gap of unknown length
2421 3456: contig of 1035 bp in length
3456 3557: gap of unknown length
3557 4704: contig of 1148 bp in length
4704 4804: gap of unknown length
4804 5826: contig of 1022 bp in length
5826 5926: gap of unknown length
5926 7885: contig of 1959 bp in length
7885 7986: gap of unknown length
7986 9240: contig of 1264 bp in length
9240 9349: gap of unknown length
9349 10577: contig of 1228 bp in length
10577 10677: gap of unknown length
10677 11851: contig of 1174 bp in length
11851 11952: gap of unknown length
11952 13062: contig of 1111 bp in length
13062 13162: gap of unknown length
13162 14336: contig of 1174 bp in length
14336 14437: gap of unknown length
14437 16140: contig of 1704 bp in length
16140 16240: gap of unknown length
16240 17988: contig of 1748 bp in length
17988 18088: gap of unknown length
18088 19777: contig of 1689 bp in length
19777 19878: gap of unknown length
19878 21119: contig of 1242 bp in length
21119 21219: gap of unknown length

```

```

* 21220 22353: contig of 1134 bp in length
* 22354 22453: gap of unknown length
* 22454 23840: contig of 1387 bp in length
* 23841 23940: gap of unknown length
* 23941 25032: contig of 1092 bp in length
* 25033 25132: gap of unknown length
* 25133 26451: contig of 1319 bp in length
* 26452 26552: gap of unknown length
* 26552 27649: contig of 1097 bp in length
* 27649 27749: gap of unknown length
* 27749 29312: contig of 1563 bp in length
* 29312 29411: gap of unknown length
* 29412 30995: contig of 1584 bp in length
* 30996 31095: gap of unknown length
* 31096 32748: contig of 1653 bp in length
* 32749 32848: gap of unknown length
* 32849 34372: contig of 1524 bp in length
* 34373 34472: gap of unknown length
* 34473 36547: contig of 2075 bp in length
* 36548 36647: gap of unknown length
* 36648 38358: contig of 1711 bp in length
* 38359 38459: gap of unknown length
* 38459 40217: contig of 1759 bp in length
* 40218 40317: gap of unknown length
* 40318 41919: contig of 1602 bp in length
* 41920 42019: gap of unknown length
* 42020 43377: contig of 1358 bp in length
* 43378 43477: gap of unknown length
* 43478 44334: contig of 1057 bp in length
* 44335 44634: gap of unknown length
* 44635 45774: contig of 1140 bp in length
* 45775 45874: gap of unknown length
* 45875 47324: contig of 1450 bp in length
* 47325 47425: gap of unknown length
* 47426 48767: contig of 1343 bp in length
* 48768 48868: gap of unknown length
* 48869 50740: contig of 1873 bp in length
* 50741 50840: gap of unknown length
* 50841 51862: contig of 1022 bp in length
* 51863 51962: gap of unknown length
* 51963 53332: contig of 1270 bp in length
* 53333 53432: gap of unknown length
* 53433 54925: contig of 1593 bp in length
* 54926 55025: gap of unknown length
* 55026 56755: contig of 1730 bp in length
* 56756 56855: gap of unknown length
* 56856 57956: contig of 1101 bp in length
* 57957 58056: gap of unknown length
* 58057 59061: contig of 1005 bp in length
* 59062 59162: gap of unknown length
* 59163 61652: contig of 2491 bp in length
* 61653 61752: gap of unknown length
* 61753 63890: contig of 2138 bp in length
* 63891 63990: gap of unknown length
* 63991 65953: contig of 1963 bp in length
* 65954 66053: gap of unknown length
* 66054 67490: contig of 1437 bp in length
* 67491 67590: gap of unknown length
* 67591 69106: contig of 1516 bp in length
* 69107 69206: gap of unknown length
* 69207 71641: contig of 2435 bp in length
* 71642 72997: contig of 1256 bp in length
* 72998 73098: gap of unknown length
* 73099 74227: contig of 1130 bp in length
* 74228 74327: gap of unknown length
* 74328 76444: contig of 2117 bp in length
* 76445 76544: gap of unknown length
* 76545 77677: contig of 1133 bp in length
* 77678 79397: gap of unknown length
* 79398 79497: contig of 1620 bp in length
* 79498 81346: contig of 1849 bp in length

```

```

* 81347 81446: gap of unknown length
* 81447 83378: contig of 1932 bp in length
* 83379 83478: gap of unknown length

Alignment Scores:
Pred. No.: 2,29e-28 Length: 150691
Score: 583.50 Matches: 115
Percent Similarity: 71.05% Conservative: 20
Best Local Similarity: 60.53% Mismatches: 48
Query Match: 16,46% Indels: 7
DB: 2 Gaps: 1

US-09-981-397A-16 (1-671) x AC131143 (1-150691)

QY 335 SerAlaThrGluGlnProGlySerLeuHisSerSerGlyLeuGlyMetCylProVal 354
DB 113822 TCTGCTACAGAAACCCGCTGTCGACAGCTCCAGGACTCCCATGGGACTGTG 113763
QY 355 GluGluSerTrpPheAlaProSerLeuGluHisProGlnGluGlnGluProSerLeu 374
DB 113762 GAGGAGTCTCGTGTTCCTTCCTCCACAGATGCCACAGAGAAATGAGCGCATGTG 113703
QY 375 GlnSerLysLeuGlnAspGlnAlaAsnTyHisLeuTyGlySerArgMetAspArgGln 394
DB 113702 CAGGCTAAACCTCAGAGAGAACCCAGTATGCTGTTGCAATATTGCCGGAATAACG 113643
QY 395 ThrLysGlnGlnProArgGlnAsnValAlaTyAsnAsnGluGlnGluArgArgArg 414
DB 113642 ACAAATACACAGCCAGCGTGAATGAGCTTACACAGAGAGAGAAAGCAAGCAAGG 113583
QY 415 ValSerHisAspProPheAlaGlnGlnArgProTyGluAsnPheGlnAsnThrGluGly 434
DB 113582 GCTCCCATGACCCCTTTGCAAGAGAGAGTGTATGAAATGTTAAGTGCAGAGAGA 113523
QY 435 LysGlyThrValTySerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGly 454
DB 113522 AAAGCTCTTCCTTATCCACAGCAACACAGTGCATGAAATGCAAGCCAGCTGCAGG 113463
QY 455 LeuThrSerGlnProGlnValLeuTyGlnAsnAsnGlyLeuTySerSerHisGlyPhe 474
DB 113462 CCAGCCAGCCAAATGAATGCGCACTTGAGACAGGAGTATTAATCATCATGAGGTTT 113403
QY 475 GlyThrArgProLeuAspProGlyThrAlaGlyProArgValTrpTyArgProIlePro 494
DB 113402 -----GGACCTACAGGTACAGAGAGTGTGTAAGGCGCAAGTGTA 113364
QY 495 SerHisMetProSerLeuHisAsnIleProValProGluThrAsnTyLeuGlyAsnThr 514
DB 113363 ACCCAATCATATATATAGCTTATATMAACTCCAGTCCAGACCACTACAGAGAGCAATA 113304
QY 515 ProThrMetProPheSerSerLeuProPro 524
DB 113303 CCCACCATGCCATACATCTCTTGACACCA 113274

RESULT 14
ARI05327 ARI05327 1873 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6096539.
DEFINITION ARI05327
ACCESSION ARI05327
VERSION ARI05327.1 GI:12818924
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1873)
AUTHORS
Gomes,B,Charles., Kasof,G.M. and Prosser,J.Caroline.
TITLE
Protein activator of apoptosis
JOURNAL
Patent: US 6096539-A 1 01-AUG-2000;
FEATURES
Location/Qualifiers
source
1..1873
BASE COUNT 471 a 531 c 518 g 353 t
ORIGIN

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Alignment Scores:

Pred. No.: 1,24e-21 Length: 1873
 Score: 448.00 Matches: 153
 Percent Similarity: 42.52% Conservative: 100
 Best Local Similarity: 25.71% Mismatches: 187
 Query Match: 12.64% Indels: 156
 Gaps: 22

US-09-981-397a-16 (1-671) x ARI05327 (1-1873)

QY 1 MetGlnProAspMetSerLeuAsnValIleuys-----11
 Db 147 CTGACACCTTCACAGCTGATGCTGCTCAAGTATGCCCCAGCGGTGCCCCCCC
 QY 12 MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyPheGluLys 30
 Db 207 TTGGTGTTCATCGAGAACTGGAGAACCGAGAGCTGCGGCAAGGCGGTTCGGCACA 266
 QY 31 ValSerLeuGlyPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50
 Db 267 GTGTTCCGGGGGCAACATAGAGAGTGGGC-----TACATGTG 305
 QY 51 ProAsnGlyIleGluHisAsnGluAlaLeuLeuGluGluAlaLysMetMetAsnArgLeu 70
 Db 306 GCGGTCAAGATCGTAAGACTCGAAGCGCATATCCAGGGAGTCAGGCGCATGCGACAGTCTG 365
 QY 71 ArgHisSerArgValIleLysLeuGluGlyValIleIleGluGluGly-----86
 Db 366 GATACCAATTCGTTGCTGGCTGAGAAAGGGTATTCGAAAGGTGCGGCTCGAGCCAA 425
 QY 87 -----LysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeuMetHisValLeu 104
 Db 426 GATCCCAAGCGCGCTGTGACTAATTCATGAGAGAGCGCTCTTTCGGGCGTGTG 485
 QY 105 LysAlaGluMetSerThrProLeuSerValLysGlyArgIleLeuGluIleLeu 124
 Db 486 CAGTCCCAAGTCCCTCGGCGCTGCGCTTTCCTTTCCTGCAAGAGTGTGCTT 545
 QY 125 GlyMetCysTyrLeuHisGlyLysGly-----ValIleHisLysAspLeuProLys 142
 Db 546 GGGATGTTTACCTGCGACGACACACCCGCTGCTGCGACCGGAGCTTCAAGCCATCC 605
 QY 143 AsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPhe 162
 Db 606 AACCTCTGCTGAGCCACAGAGCTGACGTCAAGTGGAGATTGGCTGTCCCATTT 665
 QY 163 LysMetIrrPserLysLeuAsnGluGluHisAsnGluLeuArgGluValAspGlyThr 182
 Db 666 CAGGAGGCTTCACAG-----TCAGGGACA 689
 QY 183 AlaLys---LysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLeuAsnAspAl 201
 Db 690 GGGTCCCGGGAGCCAGGGGACCCCTGGCTTACTTGGCCCAAGACTGTTGTTACCTA 749
 QY 202 AsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValAlaLeuTrrPalal 221
 Db 750 AACCGAGAGGCTTCACAGAGTGTACAGCTTCGGGATTCCTAATGTGGGCAATG 809
 QY 222 PheAlaAsnLysGlu-----ProTyrGlu-----AsnAlaIleCys 233
 Db 810 CTTCCTGGAAGAGAGTGTAGTTCACCAACCAACATCATCTGTTACGAGACAGTGTGC 869
 QY 234 GluGlnGluLeuIleMetCysIleLysSerGlyAsnArgProAspValAspAspLeuThr 253
 Db 870 AACAGGAG-----AACCGGCTTCATTGGCTGAGTGTGCC 905
 QY 254 GluTyrCysProArgGlu-----IleIleSerLeuMetLysLeuCysTrp 268
 Db 906 CAAGCGGGGCTGAGACTCCCGCTTAGAAGAGCTGAAGAGAGCTACACTGTCTGCGG 965
 QY 269 GluAlaAsnProGluAlaArgProThrPhe-----ProGlyIleGluGluLys 284

Db 966 AGCAGTAGCCCAAGACAGACCCCTCTCCAGAAATGCCCTACAAAACATGATGATGC 1025
 QY 285 PheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAspValLysSerLeu 304
 Db 1026 TTCCAG-----ATGTTGAGAACATATGATGCTGTCTTCACAGGTA 1070
 QY 305 LysLysGluTyrSerAsnGluAsnAlaValAlaValLysArgMetGlnSerLeuGlnLeuAsp 324
 Db 1071 AAGGATTTCTCTGCTCAGCTCAGACGACCAATAGAGATT-----1112
 QY 325 CysValAlaValProSerSerArgSerAsnSerAlaThrGlnGluProGlySerLeuHis 344
 Db 1113 -----TCTATCCAGAGTCA-----1127
 QY 345 SerSerGlnGlyLeuGlyMetGlyProValGluGluGluSerThrPheAlaProSerLeuGlu 364
 Db 1128 -----GGCCAAAGAGAGGACAGAAATGATGCTTTAGAGAAACCATAGAA 1172
 QY 365 HisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGluAspGluAsnTyr 384
 Db 1173 AACCAAGCACTCTCTAATGATGTCATGTTTGTAGTGGCTA-----1214
 QY 385 HisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAla 404
 Db 1215 -----AACAACTGAATCTAGAGAGACCTCCAGCTCTGTT---1250
 QY 405 TyrAsnArgGluGluGluArgArgArgValSerHisAspProPheAlaGlnIleArg 424
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 Db 1268 CCTTACCAAGAGAGACAGGAGGACAGAGAGAGAGTTCACAGCTGACAGCAGGAC 1327
 QY 444 HisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrG1 464
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 QY 464 AsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAl 484
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 QY 484 aglyProArgValTrrTyrArgProIleProSerHisMetProSerLeuHisAlaPrr 504
 Db 1416 -----CCAAAT-----CC 1423
 QY 504 oValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuProPr 524
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 Db 1544 AGTTGAGACAAACAACACTTGTGACTATGACACAGCACTGCTGC 1586

RESULT 15
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 LOCUS Sequence 1 from Patent WO0077200.
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 ACCESSION AX067676.1 GI:12329570
 VERSION
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 SOURCE
 ORGANISM human:
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1873)
 AUTHORS Gomes,B.C., Kasol,G.M. and Prosser,J.C.
 TITLE Receptor interacting protein rip3
 JOURNAL Patent: WO 0077200-A 1 21-DEC-2000;

FEATURES	Astrazeneca AB (SE)
source	location/qualifiers 1. 1.1873 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	471 a 531 c 518 g 353 t
ORIGIN	

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 25, 2003, 19:48:48 ; Search time 371 Seconds
(without alignments)
4073.021 Million cell updates/sec

Title: US-09-981-397A-16
Perfect score: 3545
Sequence: 1 MOPDMSLNVKMKSSDFLES.....ALHCCSRDLSSLIVYSON 671

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2185239 segs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu2 -TRANS=human40.cdl
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3545	100.0	2016	22	AAF86480
2	3545	100.0	2016	23	AA880489
3	3545	100.0	2617	21	AA289748
4	3545	100.0	2617	24	ABN81397
5	3545	100.0	2617	24	ABN81170
6	3539	99.8	2016	18	AAT66408
7	3513	99.1	2137	18	AAT43753
8	3505	98.9	9687	22	AA838810
9	3505	98.9	9687	22	AA838810
10	2899	81.8	3750	20	AAV99818
11	2423.5	68.4	2268	18	AAT43752
12	2423.5	68.4	2268	20	AAV99827
13	1531	43.2	2879	23	AA880491
14	521	14.7	606	21	AA280411
15	461.5	13.0	1871	22	AAK94599
16	448	12.6	1873	21	AAA47701
17	448	12.6	1873	22	AAD16312
18	446	12.6	1557	21	AAA47702
19	446	12.6	1557	22	AAAD16313
20	441.5	12.5	2140	21	AA75675
21	440.5	12.4	1887	23	ABK43722
22	440	12.4	1697	22	AAE28988
23	435	12.3	1557	21	AAZ50788
24	423.5	11.9	3876	22	AAH15762
25	410.5	11.6	2370	21	AAZ61161
26	410.5	11.6	3516	21	AAZ61784
27	410.5	11.6	3516	22	AAE99717
28	410.5	11.6	3516	22	ABL34869
29	409.5	11.6	1700	24	ABL34883
30	408.5	11.5	1774	21	AAZ61830
31	408.5	11.5	1774	22	AAZ61830
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33	408.5	11.5	2015	24	ABK62584
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35	405.5	11.4	1437	22	AAE30546
36	403.5	11.4	2355	24	ABA90356
37	397.5	11.2	2499	22	AA506739
38	377	10.6	366	21	AAE03316
39	375.5	10.6	1888	21	AAZ61671
40	375.5	10.6	1888	22	AAC99604
41	375.5	10.6	1888	24	ABL34756
42	371	10.5	1619	24	AAZ40753
43	371	10.5	1931	20	AAZ09246
44	371	10.5	1931	22	AAE30001
45	371	10.5	1931	24	AAZ40752

ALIGNMENTS

RESULT 1
ID AAF86480 standard: cDNA: 2016 BP.

AC AAF86480;
XX 28-JUN-2001 (first entry)

XX Human Receptor Interacting Protein, hRIP, coding sequence.

DE Human; Receptor Interacting Protein; hRIP; antibacterial; cytostatic;
XX antiinflammatory; gene therapy; infection; genetic disease; neoplasia;

KW Tumour necrosis factor Receptor Associated Factor-2; TRAF2; TRADD;

KW Tumour necrosis factor Receptor Associated Death Domain protein;

KW Inflammation; hypersensitivity; ss.

KW Homo sapiens.

OS

XX

Key	Location/Qualifiers
FT CDS	1..2016
FT	/*tag= a
FT	/product= "Human RIP"
XX	US6211337-B1.
XX	03-APR-2001.
XX	11-AUG-1998; 98US-0132118.
XX	23-OCT-1995; 95US-0553727.
XX	(TUDA-) TOLARIK INC.
XX	Batchwal VR, Huang J, Hsu H, Goeddel DV;
XX	WPI: 2001-334617/35.
XX	P-PSDB; AAB82091.
PT	New receptor interacting protein polypeptide having threonine in position 514 useful in screening assays for agents that modulate interaction of protein with its binding targets
PS	Disclosure: Columns 7-12; 10pp; English.
CC	The present sequence is the coding sequence for human Receptor
CC	Interacting Protein (RIP). RIP is useful in screening assays for agents that modulate the interaction of RIP with its natural binding targets, especially substrates such as Tumour necrosis factor Receptor Associated Factor-2 (TRAF2) and Tumour necrosis factor Receptor Associated Death Domain protein (TRADD). The agents are potentially useful for the treatment and diagnosis of diseases, e.g. infections, genetic diseases, neoplasia, inflammation and hypersensitivity.
XX	Sequence 2016 BP; 629 A; 446 C; 514 G; 427 T; 0 other;
SO	
Alignment Scores:	
Pred. No.:	4.2e-264
Score:	3545.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	22
	Gaps: 0
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QY	1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
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QY	21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGly 40
DB	61 GCAGACACGACGACGAGGAGCTTGGAGAGGTCTCTCTGTTTCCACAGAACCCAGGGA 120
QY	41 LeuMetIleMetLysThrValTyrLysGlyProAsnGlyIleGluHisAsnGluAlaLeu 60
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QY	61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
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QY	81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
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QY	101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
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QY	141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB	421 CCTGAATATCTCTTGTGATATATGATCTCCACATTAAGATGCGAGACCTGGCCCTTCC 480
QY	161 SerPheLysMetIlePheSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
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QY	461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
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QY	481 ProGlyThrAlaGlyProArgValTyrTyrArgProIleProSerHisMetProSerLeu 500
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XX		Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW		food supplement; medical imaging; diagnostic; genetic disorder; ss.	
KW		Homo sapiens.	
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XX		WO200175067-A2.	
FN		11-OCT-2001.	
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DD		30-MAR-2001; 2001WO-US08631.	
PE		31-MAR-2000; 2000US-0540217.	
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XX		Drmancac RT, Liu C, Tang YT;	
EI			
XX		WPI: 2001-639362/73.	
DR		P-PSDB: ABGI6302.	
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XX		New isolated polynucleotide and encoded polypeptides, useful in	
PT		diagnostics, forensics, gene mapping, identification of mutations	
PT		responsible for genetic disorders or other traits and to assess	
PT		biodiversity -	
XX			

Claim 1 SEQ ID No 16293; 103pp:English.

xx The invention relates to isolated polynucleotide (I) and
cc polypeptide (II) sequences. (I) is useful as hybridisation probes,
cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome
cc and gene mapping, and in recombinant production of (II). The
cc polynucleotides are also used in diagnostics as expressed sequence tags
cc for identifying expressed genes. (I) is useful in gene therapy techniques
cc to restore normal activity of (II) or to treat disease states involving
cc quantitating a polypeptide in tissue, as molecular weight markers and as
cc a food supplement. (II) and its binding partners are useful in medical
cc imaging of sites expressing (II). (I) and (II) are useful for treating
cc disorders involving aberrant protein expression or biological activity.
cc The polypeptide and polynucleotide sequences have applications in
cc diagnostics, forensics, gene mapping, identification of mutations
cc responsible for genetic disorders or other traits to assess biodiversity
cc and to produce other types of data and products dependent on DNA and
cc amino acid sequences. A564197-A594564 represent novel human
cc diagnostic coding sequences of the invention.
cc Note: The sequence data for this patent did not appear in the printed
cc specification, but was obtained in electronic format directly from WIPO
cc at ftp.wipo.int/pub/published_pat_sequences.
xx

Sequence 2016 BP; 629 A; 446 C; 514 G; 427 T; 0 other;

Alignment Scores:

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Score:	3545.00	Matches:	671
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
Ds:	23	Gaps:	0

US-09-981-397A-16 (1-671) x AAS80489 (1-2016)

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OY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuCysPheHisArgThrGlnGly 40
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Db 121 CTCATGATCATGAAGAACAGTGTCACAAAGGGGCCCACTGATTCAGACACACAGGCCCTC 18
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OY 161 SerPheLysMetTyrSerLysLeuAsnGluGlnHisAsnGluIleuArgIleValAsp 18
Db 481 TCTCTTAAAGATGTGGAGCAAACTGATATATGAAGGACCAATAGACTGAGGAACTGGAC 54
OY 181 GlyThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaProGluHisLeuAsnAsp 200

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|||||
541 GGCACCGCTAAGAAATGCGCGCACCTTACTCATGCGCCGAGACCTGATGAC
600
ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuThrPheAla
220
601 GTCAACGCAAAACCCACAGAGAGTGGATGGTACAGCTTGGCTGTACTCTGGGGG
660
IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGluGlnLeuIleMetCys
240
661 ATATTGGCAATTAAGAGCCATATGAATGCTATCTGTGAGCAGACAGTTGATATGTGC
720
IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle
260
721 ATAAATCTGGAGAACGCGCAGATGTGATGATCAGTACTGCTGCCCAAGAGCAAAAT
780
IleSerLeuMetLysLeuCysTyrGluAlaAsnProGluAlaArgProThrPheProGly
280
781 ATCACTCTCATGAACTCTGCTGGAGAGCGAATCCGGAACTCGGCCCATTTCTTGCC
840
IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluLysSerValGluLysAsp
300
841 ATTGAAGAAAATTTAGGCTTTTATTAACTCAATTAGAAGAAAGTGTACAGAGGAC
900
ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGlnSer
320
901 GTGAAGAGTTAAAGAAAGATATTCAAACGAAATGACGTTGTGACAGAAATGACAGTCT
960
LeuGlnLeuAspCysValAlaValAlaProSerSerArgSerAsnSerAlaThrGlnGlnPro
340
961 CTTCACTTGATTTGTGTGGCACTACCTTCACCGGTCGCAAAATTCAGCCACAGACAGCCT
1020
GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla
360
1021 GGTTCACTGCACAGTTCAGAGGACTTGGATGGTCCGTGTGAGAGAGTCCGTGGTTGCT
1080
ProSerLeuGlnHisProGlnGluLysAsnGluProSerLeuGlnSerLysLeuGlnAsp
380
381 CCTTCCCTGGAGACCCACCAAGAAAGATGAGCCACGCTGCAGAACTCCACAGAC
1140
GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArg
400
1141 GAAGCAACTACCATCTTTATGCGACCGCCATGAGCAGGACAGCAAGACAGCCCGCA
1200
GlnAsnValAlaTyrAsnArgGluGluLysArgArgArgValSerHisAspProPhe
420
1201 CAGATGTGGCTTACACAGAGAGAGAAAGAGACGAGGCTCTCCCATGACCTTTT
1260
AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValLysSer
440
421 GCACAGCAAAAGACCTTACGAGATTTTCAGAAATACAGAGGAAAGGACACTGTTATTCC
1320
SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln
460
441 AGTCAGACGACGATGATATGCACTGACACCGCCCTCAGGCTCACCAGCCAACTCA
1380
1321 AGTCAGACGACGATGATATGCACTGACACCGCCCTCAGGCTCACCAGCCAACTCA
1380
ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp
480
461 GTACTGTATCGAACAAATGATATATATAGCTCATGCTTGTGAAACAGACCACTGGAT
1440
ProGlyThrAlaGlyProArgValTrpTyrArgProIleProSerHisMetProSerLeu
500
481 CCGAGAACAGCAGGCTCCAGAGTTGTGACAGGCCCAATTCAGATATGCTGAGTGG
1500
1441 HisAsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSer
520
501 CATATATCCAGCTGCTGAGAGCACTATCTAGAAATACACCCACCATGCACTTCCAC
1560
1501 SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAspSerThrGlyIleGln
540
521 TCCCTTGCACCAACAGATGAAATCTATAAATATACATATACAAATAGTACTGCAATCAG
1620
1561 IleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerLeuLeuAspSerThr
560
|||||

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Db 1621 ATTGAGCCCTACATTTATATGAGATTTGGTGGAGAGTTCATCCTACTACAGACACA 1680
Qy 561 AsnThrAsnPheLysGluGluProAlaAlaLysTyrGlnAlaIlePheAspAsnThrPhe 580
Db 1681 AATACGAACTTAAAGAACAGCCAGCTGCTAAGTACCAAGCTATCTTGTATATATCCACT 1740
Qy 581 SerLeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsn 600
Db 1741 ACTGTAGCAGATAAACACTGTCAGCCCAATCAGAGAAATCTGGAAAGACACTGAGAAAC 1800
Qy 601 CysAlaAlaGlyLysGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu 620
Db 1801 TGTGCCCGTAAACTGGCTGCTCACAGTCTCGATGTGATGAAATTCACCATCATCATAG 1860
Qy 621 ArgAspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTrpValMetArgGluGly 640
Db 1861 CGAGATGAGCTAAAGAAAGGTTTACAGATGCTCCAAAGTGGGTGATGAGGAGGAC 1920
Qy 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
Db 1921 ATAAAGGAGCCACGAGTGGGAAAGCTGGCCAGCGGCTCCACAGCTTCCAGATCGAC 1980
Qy 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
Db 1981 CTTCTGAGCAGCTGATTTACGTGACCGAGAAC 2013

RESULT 3
AA289748
ID AA289748 standard, DNA; 2617 BP.
XX
AC AA289748;
XX
AC 05-MAY-2000 (first entry)
XX
DE Human RIP-1 nucleotide sequence.
XX
KW RIP-1; RalBP; RLIP; antisense inhibitor; anti-inflammatory; cytostatic;
XX anti-infective; diagnose; prevent; treatment; tumour formation; ds.
XX
OS Homo sapiens.
XX
PN US6020198-A.
XX
PD 01-FEB-2000.
XX
PF 25-SEP-1998; 98US-0161443.
XX
PR 25-SEP-1998; 98US-0161443.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowseart LM;
XX
PT WPI: 2000-146889/13.
XX
DR P-PSDB: AAT78502.
XX
PT Antisense inhibition of human RIP-1 expression, useful for diagnosing,
XX preventing and treating conditions such as inflammation -
XX
PS Claim 1; Column 29-36; 26pp; English.
XX
CC This sequence represents the human RIP-1 nucleotide sequence. RIP-1 (also
CC known as RalBP1 and RLIP) is a GTPase activating protein (GAP) thought to
CC be a downstream target of Ral. The invention relates to RIP-1 antisense
CC phosphorothioate oligonucleotides with anti-infective, anti-inflammatory
CC and cytostatic activity. The oligonucleotides are RIP-1 antisense
CC inhibitors and are used in the diagnosis, prevention and treatment of
CC conditions associated with RIP-1 expression. Conditions associated with
CC RIP-1 expression include various infections, inflammation and tumour
CC formation.
XX
SQ Sequence 2617 BP; 794 A; 586 C; 659 G; 574 T; 4 other:

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Alignment Scores:

Pred. No.: 5.88e-264 Length: 2617
Score: 3545.00 Matches: 671
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-981-397a-16 (1-671) x AAZ89748 (1-2617)

QY 1 MetClnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
DB 1 ATGCACACAGACAGTCTTGAATGATTAAGTGAATCAATCCAGTGAATCTCTCTGAGAGT 60
QY 21 AlaGlnLeuAspSerGlyGlyPheGlyLysValSerLeuGlnSerPheHisArgThrGlnGly 40
DB 61 GCAGAACTGGACAGCGAGGCTTTGGAGAGGTCTCTGTCTTTCCACAGAACCCAGGGA 120
QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnGlnIleGlnHisAsnGlnValAlaLeu 60
DB 121 CTCATGATCATGAAGAACAGTGTACAGAGGGCCCAATGCATTTGAGCACACAGAGCCCTC 180
QY 61 LeuGlnGlnAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
DB 181 TTGGAGAGGCGGAGATGATGAAACAGACTGACACAGCCGGGTGTGAACTCTCTGGGC 240
QY 81 ValIleIleGlnGlnGlyLysTyrSerLeuValIleMetGlnTyrMetGlnLysGlyAsnLeu 100
DB 241 GTCTCATATAGAGAGGAAAGTACTCCCTGGTGTGATGATGATGAGAGAGGCAACTG 300
QY 101 MetHisValLeuLysAlaGlnMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
DB 301 ATGCACGTGGCGAAGCGCAGATGAGTACTCCGCTTCTCTAAGAGAGATATTTTG 360
QY 121 GlnIleIleGlnGlyMetCysTyrLeuHisGlnLysGlyValIleHisLysAspLeuLys 140
DB 361 GAAATTCATTGAAGAAATGCTTACTACTGAAAGAGCGGATACACAAAGACTCTGAG 420
QY 141 ProGlnAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB 421 CTTGAAATATCTTGTGTGATTAATGACTTCCACATTAAGATGCGAGACTGGCCCTGGC 480
QY 161 SerPheLysMetIlePheLysLeuAsnAsnGlnLysHisAsnGlnLeuArgGlnValAsp 180
DB 481 TCTTTAAGATGTGAGCAAACTGATATGAAGACACATGAGCTGAGGAGTGGAC 540
QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGlnHisLeuAsnAsp 200
DB 541 GGCACCCCTTAAGAAATGGCGGCCCTTACTACTACATGGCGCCGACCTGAATGAC 600
QY 201 ValAsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValIleLeuTrpAla 220
DB 601 GTCAACCCAAAGCCCAAGAGAGTGGATGTGACGCTTGTGTGATGCTCTGGGCG 660
QY 221 IlePheHisAsnLysGlnProTyrGlnAsnAlaIleCysGlnGlnGlnIleuIleMetCys 240
DB 661 ATATTTCGAATAGAGGCCATATGAATGCTATCTGTGAGCAGCAAGTTGATATGCGC 720
QY 241 IleLysSerGlnAsnArgProAspValAspAspIleThrGlnTyrCysProArgGlnIle 260
DB 721 ATAAAACTGGGAGACAGCCAGATGTGATGATCACTGAGTCTGCCCAAGGAATTT 780
QY 261 IleSerLeuMetLysLeuGlnTyrGlnAlaIleAsnProGlnAlaArgProThrPheProGly 280
DB 781 ATCGTCTCATGAGAGCTCTGCTGGAGCCGATCCGAGAGCTCGGCGACATTTCTCGGC 840
QY 281 IleGlnGlnLysPheArgProPheTyrLeuSerGlnLeuGlnGlnSerValIleGlnLys 300
DB 841 ATTGAAGAAAAATTAGCCCTTTTATTTAAGTCAATTAGAAGAAAGTGTGAAGAGAC 900
QY 301 ValLysSerLeuLysGlnTyrSerAsnGlnAsnAlaValValLysArgMetGlnSer 320
DB 901 GTGAAGAGTTTAAAGAAAGATATTCAACGAAATGCGAGTTGTGAAGAGAAATGCAGTCT 960

QY 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnPro 340
DB 961 CTTCACTGATGATTTGTGTGGCAGTACTTCAAGCCGGTCAATTTACGCCACAGACAGCTT 1020
QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGlnGlnSerTrpPheAla 360
DB 1021 GGTTCACCTGCACAGTCCACAGGAGCTGGATGGATGGCTCTGTGAGAGAGTCTGGTTGCT 1080
QY 361 ProSerLeuGlnHisProGlnGlnGlnLysGlnLysProSerLeuGlnSerLysLeuGlnAsp 380
DB 1081 CTTTCCTGGAGCACCACCAAGAGAGATAGCCACGCTCGCAGAGTAACTCCAGAC 1140
QY 381 GlnAlaAsnTyrHisLeuTyrGlnTyrSerArgMetAspArgGlnTrpLysGlnIleProArg 400
DB 1141 GAAGCCAACTGCCATCTTTATGGACGCCGCTGGACAGCGAGCAAGAACAGCAGCCAG 1200
QY 401 GlnAsnValAlaTyrAsnArgGlnGlnGlnLysArgArgArgValSerHisAspProPhe 420
DB 1201 CAGAAATGGCTTACAAACAGAGAGAGAGAAAGAGACGACGAGTCTCCATGACCTTTT 1260
QY 421 AlaGlnGlnArgProTyrGlnAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSer 440
DB 1261 GCACAGCAAAAGACCTTACGAAATTTTCAGAAATACAGAGGAGGAAAGGACACTGTTATTC 1320
QY 441 SerAlaIleSerHisGlnAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
DB 1321 AGTCGACGACATCTATGTAATGCAAGTGCACACGCCCTCAGGCTCACCAGCCAACTCAA 1380
QY 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
DB 1381 GTACGTATCAAGAACATGATTTATATAGCTACATGGCTTTGAGACAGACCACTGGAT 1440
QY 481 ProGlyThrAlaGlyProArgValTrpTyrArgProIleProSerHisMetProSerLeu 500
DB 1441 CCAGAGACAGAGGTCCCGAGATTGGTACAGGCCAAATCCAAAGCATATCTCAATGTG 1500
QY 501 HisAsnIleProValProGlnThrAsnTyrLeuGlnLysAsnTrpProThrMetProPheSer 520
DB 1501 CATATATCCAGAGTCCGAGACCACTATGTAGGAATACACCCACCATCCATTCAGC 1560
QY 521 SerLeuProProThrAspGlnSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
DB 1561 TCTTTGCCACACAGATGATTAATAATATACATATACATATAGTACGCTGCTAG 1620
QY 541 IleGlyAlaTyrAsnTyrMetGlnIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
DB 1621 ATTGAGGCTTCAATTTATATGAGATGTGGTGGACGAGTTCATCTACTAGACAGCACA 1680
QY 561 AsnThrAsnPheLysGlnGlnProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThr 580
DB 1681 AATACGAACTTCAAGAGAGACGAGCTGTAAGTACAGCTATCTTTGATTAATACCACT 1740
QY 581 SerLeuThrAspLysHisLeuAspProIleArgGlnAsnLeuGlnLysHisTrpLysAsn 600
DB 1741 AGTCGACAGGATTAACACTCTGACCCCATACAGGAAATCTGGGAAAGACACTGGAAAAAC 1800
QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGlnIleAspHisAspTyrGln 620
DB 1801 TGTGCCCTTAAACGGGCTTTCACACAGTCTCAGATTGATGAATTTGACCAAGCATATCAG 1860
QY 621 ArgAspGlyLeuLysGlnLysValTyrGlnMetLeuGlnLysTrpValMetArgGlnGly 640
DB 1861 CGAGATGACTGAAAGAAAGGTTTACCAGATGCTCCCAAAAGGTGGTATATAGGGAAGGC 1920
QY 641 IleLysGlyAlaThrIleValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
DB 1921 ATAAAGGAGCGCAGGTGGGAGAGTGGCCAGGCGCTCCACAGTGTTCAGAGATGAC 1980
QY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
DB 1981 CTTCTGAGCAGCTTGAATTTACGTACGCCAGAAC 2013

RESULT 4
ID ABN81397
ABN81397 standard; CDNA; 2617 BP.
AC ABN81397;
DE 03-SEP-2002 (first entry)
XX Human RIP encoding cDNA.
XX
XX Human; RIP; cell death protein RIP; receptor interacting protein;
XX serine/threonine protein kinase; enzyme; immunosuppressive; cardiac;
XX cerebroprotective; neurotrophic; antiparkinsonian;
XX virucide; antiarthritic; antirheumatic; antidiabetic; dermatological;
XX death receptor; caspase; necrosis; immune system; autoimmune disease;
XX multiple sclerosis; diabetes; rheumatoid arthritis; infection; viral;
XX neurological disease; Alzheimer's disease; Parkinson's disease; viral;
XX signal transduction; gene; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 1..2016
FT /*tag= a
FT /product= "RIP"
XX
XX W0200236148-AZ.
XX
XX 10-MAY-2002.
XX
XX 26-OCT-2001; 2001WO-EP12440.
XX
XX 02-NOV-2000; 2000DE-1054279.
XX
XX (APOF-) APOTECH RES & DEV LTD.
XX
XX Tschopp J, Holler N;
XX
XX WPI; 2002-519224/55.
XX
XX P-PSDB; ABB83794.
XX
XX
XX Use of a death receptor ligand or receptor interacting protein to
XX induce necrotic cell death, useful for treating e.g. autoimmune
XX disease, also their inhibitors
XX
XX
XX Disclosure; Fig 8; 56pp; German.
XX
XX The invention relates to the use of a ligand (I) of the death receptor
XX or its functional derivative, for inducing caspase-independent (i.e.
XX necrotic) death (CID) in cells, especially those of the immune system.
XX (I) are used to induce CID of peripheral blood lymphocytes, especially
XX activated T cell for treatment of autoimmune diseases. Also CID can be
XX inhibited by using agents (II) that bind to (I), or agents (III) that
XX inhibit function of RIP (receptor-interacting protein), particularly for
XX treatment of autoimmune diseases (e.g. multiple sclerosis, diabetes,
XX lupus or rheumatoid arthritis); cardiac infarction; cerebral stroke; or
XX neurological diseases (Alzheimer's or Parkinson's). (III) can also be
XX used to treat diseases associated, at least in part, with pathological
XX hypernecrosis and viral infections. The ligand modulates signal
XX transduction through RIP or the death receptor. The present sequence is
XX that of the human cell death protein RIP, a serine/threonine kinase,
XX encoding cDNA of the invention.
XX
XX Sequence 2617 BP; 794 A; 586 C; 659 G; 574 T; 4 other;

Alignment Scores:

Pred. No.: 5,88e-264
Score: 3545.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 24

Length: 2617
Matches: 671
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-981-397A-16 (1-671) x ABN81397 (1-2617)

QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
DB 1 ATGCACACGACATGCTCTTGATGTCATTAAGATGAATCAATCCAGACTCTCCGAGAGT 60
QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyCysPheHisArgThrGlnGly 40
DB 61 GCAGAACTGACAGCGGAGGAGGCTTTGGAAAGGTCTCTGTGTTCCACAGAAACCGAGGA 120
QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnCysIleGluHisAsnGluAlaLeu 60
DB 121 CTCATGATCATGAAAAACAGTGTACAAAGGGCCCACTCATTTGACCAACAGAGGCCCTC 180
QY 61 LeuGluGluAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
DB 181 TTGGAGAGGCCAATAATGATGACAGCTGACACACACCGGAGTGGTAAAGCTCCTGGGC 240
QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
DB 241 GTCATCATAGAGGAAGGAGAGTACTCCTGGTGAATGAGTACATGAGAGGAGGACCTG 300
QY 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleLeu 120
DB 301 ATGCACGCTGCGAAAGCCGAGATGACTCCGCTTCTGTAAAAGAGGATTAATTTTG 360
QY 121 GluIleIleGluGluMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
DB 361 GAATCATTTGAAAGAAATGCTACTTACATGGAAAAAGCCGATACACAGAGCCTGAG 420
QY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB 421 CCTGAATAATATCCTTGATATGATGATCCATTAAGATTAAGATGAGGAGCCTGCTTCC 480
QY 161 SerPheLysMetThrSerLysLeuAsnAsnGluGluHisAsnGluLeuArgIleValAsp 180
DB 481 TCCCTTAAGATGTGGACCAACTGAATATGAAGACCAATAGAGCTGAGGAAATGTGAC 540
QY 181 GlyThrAlaLysLysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLysAsnAsp 200
DB 541 GGCACCGCTAAGAAATATGGCGGACCTCTACTACATGAGCGCCGAGACCTGATATAC 600
QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuThrPala 220
DB 601 GTCAACGCAAGCCCAAGAGAGATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 IlePheAlaAsnLysGluProThrGluAsnAlaIleCysGluGluGluLeuIleMetLys 240
DB 661 ATATTTCGAAATTAAGGACCATATGAAAAATCTATCTGTGACACGACTTGATTAATGTC 720
QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
DB 721 ATAAATCTGGGAACAGGCCAGATGTGATGATGATGATGATGATGATGATGATGATG 780
QY 261 IleSerLeuMetLysLeuGlyTrpGluAlaAsnProGluAlaArgProThrPheProGly 280
DB 781 ATCACTCATATGAACCTGCTGCGAAGCAATCCGGAAGCTCGCGCAATTTCTCTGCG 840
QY 281 IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluLysp 300
DB 841 ATTTGAAGAAAAATTTAGGCTTTTATTTAATCAATTAGAAGAAAGCTGAGAAAGAGAC 900
QY 301 ValLysSerLeuLysGlyLysTyrSerAsnGluAsnAlaValValLysArgMetGlnSer 320
DB 901 GTGAAGAGTTTAAAGAAAGAGATATTCANAGCAAAATGCAATGTGTGAAGAGATGCACT 960
QY 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
DB 961 CTTCAACTGATGTGTGGACATACCTTCAACCGCGTCAAAATATTCAGCCACAGACAGCT 1020
QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerThrPheAla 360
DB 1021 GGTTCACTGCACAGTTCCAGGAGCTTGAGTGGGTCTCTGTGAGAGAGTCTCGTTTCT 1080

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OY 361 ProSerLeuGIuHISProGIuGIuAsnGIuProSerLeuGlnSerLysLeuGlnAsp 380
DB 1081 CCTTCCCTGGAGACCCACAGAAAGATGAGCCACCTGCGAGAGTAACTCCAGAC 1140
OY 381 GIuAlaAsnTYRHSLeuTYRGIYSerArgMetAspArgGlnTYRHSLeuGlnProArg 400
DB 1141 GAAGCCAACTACATCTTATGGCAGCCGATGAGCAGACGAGAAACAGCAGCCAGCA 1200
OY 401 GlnAsnValAlaTYRAsnArgGIuGIuArgArgArgValSerHisAspProPhe 420
DB 1201 CAGAAATGGGCTTCAACAGAGAGAGAGAAAGAGACAGGCTCCCATGACCTTTT 1260
OY 421 AlaGlnGlnArgProTYRGIuAsnPhelGlnAsnTYRGIuLysGIuTYRValTYRser 440
DB 1261 GCACAGCAAAAGCTTACGAGAAATTTCCAGAAATACAGAGGAAAAGCACTGTTATTCC 1320
OY 441 SerAlaAlaSerHisGIuAsnAlaValHisGlnProSerGIuLeuTYRserGlnProGln 460
DB 1321 AGTCAGAGCCATGATGTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
OY 461 ValLeuTYRGIuAsnAsnGIuLeuTYRserSerHisGIuPheGIuTYRArgProLeuAsp 480
DB 1381 GTACTGATTCAGAACAAATGATTAATATGATGATGATGATGATGATGATGATGATGAT 1440
OY 481 ProGIuTYRAlaGIuProArgValTYRArgProLeuProSerHisMetProSerLeu 500
DB 1441 CCAGAGACAGCAGCTCCAGAGCTTTGGTACAGGCCAATTCAGATCATATGCTTGTG 1500
OY 501 HisAsnIleProValProGIuTYRAsnTYRLeuGIuAsnTYRProThMetProPheSer 520
DB 1501 CATATATATCCAGTCCGCTGAGACCACTATCTAGAAATFACACCCATGCTGATTCAGC 1560
OY 521 SerLeuProProThMetAspGIuSerLysTYRThrIleTYRAsnSerThGIuIleGln 540
DB 1561 TCTTGGCCACCAAGATGATTAATAAATATACCAATATCAATATGATGATGATGATGAT 1620
OY 541 IleGIuAlaTYRAsnTYRMetGIuIleGIuTYRserSerSerLeuLeuAspSerThr 560
DB 1621 ATTGAGAGCTTCAATTAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
OY 561 AsnThrAsnPhelLysGIuLysProAlaAlaLysTYRGIuAlaIlePheAspAsnThrThr 580
DB 1681 AATACGAACCTTCAAAAGAGAGCCAGCTCTAAGTCAAGCTATCTTGAATATACCACT 1740
OY 581 SerLeuThrAspLysHisLeuAspProIleArgGIuAsnLeuGIuLysHisTYRAsn 600
DB 1741 AGCTGAGGATTAACACCTGAGCCCAATCAGGGAAATCTGGGAAACACTGGAATAAC 1800
OY 601 CysAlaArgLysLeuGIuPheTYRGIuSerGlnIleAspGIuIleAspHisAspTYRGIu 620
DB 1801 TGTGCCCTTAACCTGGCTTCCACAGCTCAGATGATGATGATGATGATGATGATGATGAT 1860
OY 621 ArgAspGIuLeuLysGIuLysValTYRGIuMetLeuGlnLysTYRValMetArgGIuLys 640
DB 1861 CGAGATGAGCTGAAGAAAGAGGTTTACAGATGCTCCAAAGTGGTGATGAGGGAAGGC 1920
OY 641 IleLysGIuAlaTYRValGIuLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660
DB 1921 ATAAAGGAGCCAGCGTGGGAGAGCTGGCCAGGCGCTCCACCACTGTTCCAGAGATCAG 1980
OY 661 LeuLeuSerSerLeuIleTYRValSerGlnAsn 671
DB 1981 CTTCGAGACCTTCATTTACGTACGCCAGAAC 2013

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RESULT 5
ABK51170
ID ABK51170 standard; cDNA; 2617 BP.

ABK51170;

30-JUL-2002 (first entry)

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DE cDNA encoding human cellular kinase RIP protein.
XX
KW Human; virulence; cytomagalovirus infection; CMV; cellular kinase; RICK;
KW RIP; Nck-interacting kinase; MKK3; SRPK-2; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2016
FT /tag=a
FT /product="Human cellular kinase RIP"
PN EP1201765-A2.
PD 02-MAY-2002.
XX
XX 15-OCT-2001; 2001EP-0124604.
XX
XX 16-OCT-2000; 2000US-240750P.
XX
XX (AXXI-) AXIIMA PHARM AG.
XX
XX Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
XX P-PSDB; AU080370.
XX
XX WPI; 2002-373930/41.
XX
XX P-PSDB; AU080370.
XX
XX Identifying agents for treatment or prevention of cytomagalovirus
XX infection, comprises contacting test compound with cellular kinase and
XX detecting change in cellular kinase activity.
XX
XX Disclosure: Page 24-27; 49pp; English.
XX
XX The present invention relates to a new method for identifying compounds
XX for treating and/or preventing cytomagalovirus (CMV) infection and/or
XX related diseases. The method of the invention comprises contacting a
XX test compound with at least one of the cellular kinases RICK, RIP,
XX Nck-interacting kinase, MKK3 and SRPK-2 and detecting any change in
XX kinase activity. The method of the invention can be used to treat and/or
XX prevent CMV infections and related diseases. Oligonucleotides that can
XX detect the specified kinases can also be used for diagnosis of infection.
XX The present nucleic acid sequence encodes the human cellular kinase RIP
XX protein of the invention, as described above.
XX
XX Sequence 2617 BP: 794 A: 586 C: 659 G: 574 T: 4 other.
XX
XX Alignment Scores:
XX Pred. No.: 5.88e-264 Length: 2617
XX Score: 3545.00 Matches: 671
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-981-397A-16 (1-671) x ABK51170 (1-2617)
OY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSer 20
DB 1 ATGCACACGACATGCTCTTGAATGTCATTAAAGATGAATCCAGATGATCTTCGAGAGT 60
OY 21 AlaGlnLeuAspSerGIuLysPheGIuLysValSerLeuCysPheHisArgTYRGIuLys 40
DB 61 GCAGAGACTGGACAGCGAGGCTTGGAGAGGTCTCTGTGTTCACAGAACCCAGGGA 120
OY 61 LeuMetIleMetLysTYRValTYRGIuLysGIuProAsnCysIleGlnHisAsnGIuAlaLeu 60
DB 121 CTGATGATCATGAAGAAAGCTGATACAGAGGCCCAACTCATTTGAGACAAAGAGGCCCTC 180
OY 61 LeuGIuGIuAlaLysMetMetAsnArgLeuArgHisSerArgValValLysLeuLeuGIu 80
DB 181 TTGGAGAGGCGGAAGATGATGAACAGACTGAGACACAGCCGGGTGGTGAAGCTCTCGGCG 240
OY 81 ValIleIleGIuGIuLysLysTYRserLeuValMetGIuTYRmetGIuLysGIuAsnLeu 100

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Db	241	GTGATCATAGAGGAAGGGAAGTACTCCCTGGTGAAGGATGCAATGGAAGGCAACTG	300
OY	101	MethiValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu	120
Db	301	ATGCACGCTGTGAAGAGCCGAGATGAGTACTCCGCTTCTGTGAAAAAGAGATATTTTG	360
OY	121	GluIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys	140
Db	361	GAATCATTTGAAGGATGCTGCTACTTACATGTGAAAAAGCGGTGATACAAAGACCTGGAAG	420
OY	141	ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla	160
Db	421	CCTGAAATATTCCTTGTGATATGACTTCCACATTAGATCGGACGACTGGCCCTTCC	480
OY	161	SerPheLysMetTrpSerLysLeuAsnAsnGluLysHisAsnGluLeuArgGluValAsp	180
Db	481	TCCTTTAAGATGTGAGCAAACTGMAATATAGAGGCAACATGTAGCTGAGGAAGTGGAC	540
OY	181	GlyThrAlaLysLysAsnGlyGlyThrLeuArgTyrMetAlaProGluHisLeuAsnAsp	200
Db	541	GGCACCGCTAAGAAAGATGGCGGCGACCTCTACTACATAGCGGCCCGGACACTGATATAC	600
OY	201	ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValIleuTrpAla	220
Db	601	GTCACAGCAAAAGCCGACAGAGAAGCGGATGTACACCTTGGTGTGATCTCTGGCGG	660
OY	221	IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGluIleMetCys	240
Db	661	ATATTGTGAATTAAGGACCATATGAAATCTATCTGTGAGCAGCATGATATATGTGC	720
OY	241	IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle	260
Db	721	ATAAATCTGGGACAGGCGAGATGTGATGCATCACTAGTACTGCCCAAGGAATT	780
OY	261	IleSerLeuMetLysLeuCysTyrGluAlaAsnProGluAlaArgProThrPheProGly	280
Db	781	ATCATGCTCAAGAAGCTCTGCTGGAGAACGAAATCGGAGAGCTGGCCACATTTCTGGC	840
OY	281	IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluLysAsp	300
Db	841	ATTGAGAAAAATTAGGCTTTTATTATTAGTCAATTAGAAAGAAAGTGTAAGAGAGAC	900
OY	301	ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValIleLysArgMetGlnSer	320
Db	901	GTTGAAGATTTAAAGAAAGACTATTCCAACCAAAATGCAGATTGTCAAGACGATCAGCT	960
OY	321	LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro	340
Db	961	CTTCAACTGTAATTGTGTGGCAGTACTTCAAGCCGGTAAATTACGACACAGAACAGCTT	1020
OY	341	GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla	360
Db	1021	GGTTTCACATGCACAGTCCACAGGAGCTGGAGTGGTCTCTGGAGAGATCTCTGGTTGCT	1080
OY	361	ProSerLeuGluLysHisProGlnGluAsnGluProSerLeuGlnSerLysLeuGlnAsp	380
Db	1081	CTTTCCTCCGTGGAGCAACCAAGAAGAGATAGCCACCTGCGAGAGTAACTCCAAAGAC	1140
OY	381	GluAlaAsnArgHisLeuTyrGlySerArgMetAspArgGlnTrpLysGlnGlnProArg	400
Db	1141	GAAGCAACTACCAATCTTATGGCAGCCGCGATGGACAGCAGAGAAACACAGCCACAGA	1200
OY	401	GlnAsnValAlaIleArgAsnArgGluGluGluArgArgArgValSerHisAspProPhe	420
Db	1201	CAGAAATGGCTTACCAACAGAGAGAGAAAGAGAGCCAGCGTCTCCATGACACTTTT	1260
OY	421	AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer	440
Db	1261	GCACAGCAAAAGCTTACGAGAAATTTTCAGAAATACAGAGGAAAAAGCATTGTTATTC	1320
OY	441	SerAlaAsnSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln	460

Db	1321	AGTGCAGCCACTGATGTGAATGACAGTGCACCAACGCCCTCAGGGCTCCACCAGCCAACTTCAA	1380
QY	461	ValLeuTyrgInAsnAsnGlyLeuTySerSerHisGlyThrIleArgProLeuAsp	480
Db	1381	GTACTGTATCCAGAAACATGATGATTTATATAGCTACATGGCTTTGGACAAAGACCTGGAT	1440
QY	481	ProGlyThrIleArgIleProArgValTyrPyrArgProIleProSerHisMetProSerLeu	500
Db	1441	CCAGSAAACAGCAGGTCGCCAGAGTTGGTACAGGCCAAATCCAAATCATATCCCTAGCTCG	1500
QY	501	HisAsnIleProValProGlyThrAsnTyrrLeuGlyAsnThrProTrpMetProPheSer	520
Db	1501	CATATATATCCAGTGCCTCGAGACCACTATCTAGSAAATACACCACCATGCCATTGACG	1560
QY	521	SerLeuProProThrAspGluSerIleuTySerTyrrIleTyrrAsnSerThrGlyIleGln	540
Db	1561	TCCTTGGCCACCAACAGATGAATCTATATAAAATATACATATCAATACATAGTACGCAATTCAG	1620
QY	541	IleGlyAlaTyrrAsnTyrrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThr	560
Db	1621	ATTGGAGGCTCTACAATTATATGAGATTGGTGGACGAGTTATCTACTACTAGACAGACACA	1680
QY	561	AsnThrAsnPhelTySerGluProAlaIleLysTyrrGlnAlaIlePheAspAsnThrThr	580
Db	1681	AATACGAACTTCAAAGAGAGAGCCAGCTGCTAAATGACCAAGCTATCTTTGATTAATATCACT	1740
QY	581	SerLeuThrAspPheHisLeuAspProIleArgGlnAsnLeuGlyIleHisTrpLysAsn	600
Db	1741	AGCTGCAGCGATAAACACCTGTGACCCCAATCGAGGAAATATCGGAGAAAGCACATGGAAAAAC	1800
QY	601	CysAlaArqLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrrGlu	620
Db	1801	TGTGCCCTTAACCTGGGCTTCACACAGTCTCAGATTGATGAATGTACCATGACATGATGAG	1860
QY	621	ArgAspGlyLeuLysGluLysValIleTyrGlnMetLeuGlnLysTrpValMetArgGluGly	640
Db	1861	CGAGATGGACGTGAAGAAAGAGTTTACCCAGATGCTCCAAAAGTGGGATGATGAGGGAAGGC	1920
QY	641	IleLysGlyAlaThrValGlyLysLeuAlaGlnIleLeuHisGlnCysSerArgIleAsp	660
Db	1921	ATTAAGGAGGACGAGGTGGGAGAGCTGGCCGACGGCGTCCACACGATGTTCAGGATGAC	1980
QY	661	LeuLeuSerSerLeuIleTyrrValSerGlnAsn	671
Db	1981	CTTCGACACAGCTTGATTTACGTGACGCCAGAAC	2013
RESULT 6			
AAT66408			
ID	AAT66408	standard; cDNA, 2016 BP.	
XX	AAT66408;		
XX			
DT	20-JUL-1997	(first entry)	
XX			
DE	Human receptor interaction protein cDNA.		
XX			
KW	Receptor interaction protein; RfP; tumour necrosis factor;		
KW	signal transduction; neoplasia; hypersensitivity; inflammation;		
KW	diagnosis; therapy; ds.		
OS	Homo sapiens.		
XX			
PN	WO9715586-A1.		
XX			
PD	01-MAY-1997.		
XX			
PF	17-OCT-1996;	96WO-US1677B.	
XX			
PR	23-OCT-1995;	95US-0553727.	
XX			
PA	(TULSA-) TULARIK INC.		
XX			
PI	Batchwal VR, Goeddel DV, Hsu H, Huang J;		

xx WPI: 1997-258948/23.
DR P-PSDB: AAM15461.
xx
xx CDNA encoding human receptor interaction protein or its kinase
PT domain - useful for identifying lead compounds, and for development
PT of therapeutic and diagnostic agents that modulate hrp activity or
PT signal transduction
xx
xx Claim 2: Page 11-13: 22pp; English.
xx
xx A CDNA clone (AAT66408) codes for human receptor interaction protein
CC (RIP) (AAM15461), a novel kinase involved in tumour necrosis factor
CC signal transduction. RIP CDNA can be isolated from a human CDNA
CC libraries (e.g. from umbilical vein endothelial cells) using probes
CC and primers contg. part of the 2016 bp sequence. RIP nucleic acids
CC can be incorporated into cells for expression and screening, or
CC into transgenic animals for functional studies (e.g. the efficacy
CC of candidate drugs for disease associated with expression of RIP).
CC They can also be used as probes e.g. to detect RIP genes and gene
CC transcripts, as primers, in gene therapy applns., and to produce
CC RIP polypeptides (esp. the kinase domain).
xx
SQ Sequence 2016 BP: 629 A; 446 C; 515 G; 426 T; 0 other:

Alignment Scores:
Pred. No.: 1-22e-263 Length: 2016
Score: 3539.00 Matches: 670
Percent Similarity: 99.85% Conservative: 0
Best Local Similarity: 99.85% Mismatches: 1
Query Match: 99.83% Indels: 0
Gaps: 0
DB: 18

US-09-981-397a-16 (1-671) x AAT66408 (1-2016)

Db 541 GGACACCGTAAAGAAAGATGGCGGACCCCTTACTACATGAGCGCCGACACCTGAATGAC 600
Qy 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValValLeuTrpAla 220
Db 601 GTCAACGGCAAGCCACAGAGAGATGGATGTGACACTTGGCTGTGACTCTGGGCG 660
Qy 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGluIleMetCys 240
Db 661 ATATTGGCAATTAAGAGACCATATGAATGCTATCTGTGAGACACCATTTGATATGTC 720
Qy 241 IleLysSerGlyAsnArgProAspValAspSpleTherGluTyrCysProArgGluIle 260
Db 721 ATAAATGTGGGACAGCCGAGATGTGATACATCATGTGATCTGCCCAAGAAATTT 780
Qy 261 IleSerLeuMetLysLeuCysTrpGluAlaAsnProGluAlaArgProThrPheProTyr 280
Db 781 ATCACTCATGAAACCTGTGGGAAACGAATCCGGAACCTGGCCGACATTTCTTCGTC 840
Qy 281 IleGluGluLysPheArgProPheTyrLeuSerGlnLeuGluGluSerValGluGluAsp 300
Db 841 ATTGAGAAATAATTAGGCCCTTTTATTAGTCAATTAGAAAGAAAGTGTAGAGAGAC 900
Qy 301 ValLysSerLeuLysLysGluTyrSerAsnGluAsnAlaValValLysArgMetGlnSer 320
Db 901 GTGAAGACTTTAAAGAAAGAGTATTCAAACGAAATGCAGTTGTGAAGAGATGCAGTCT 960
Qy 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
Db 961 CTTCACTTGTATGTGTGGAGTACCTTCAAGCCGCTCAAAATTCAGCCAGAAACACCT 1020
Qy 341 GlySerLeuLysSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla 360
Db 1021 GGTTCACCTGCACAGTCCACAGGACTTGGATGGTCTCTGTGAGAGAACTCTGGTTTCT 1080
Qy 361 ProSerLeuGlnHisProGlnGluAsnGluProSerLeuGlnSerLysLeuGlnAsp 380
Db 1081 CCTTCCTGTGAGACCCACAGAAAGAGATGAGCCACCTGTGACAGTAACTCCAGAAC 1140
Qy 381 GluAlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGluProArg 400
Db 1141 GAAGCCAACTACCATTTTATGAGCGCGCATGGACGAGACGAAACAGACGACCCGGA 1200
Qy 401 GlnAsnValAlaTyrAsnAsnArgGluGluLysArgAsnValSerHisAspProPhe 420
Db 1201 CAGAAATGGCTTACAAACAGAGAGAGAAAGAGACGAGGTCTCCCATGACCTTTT 1260
Qy 421 AlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer 440
Db 1261 GCACAGCAAAAGACCTTACGAGATTTTCAGATACAGAGGGAAGGACACTGTTATTC 1320
Qy 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
Db 1321 AGTCGACGACATGATGTAATGCACTGCACGACCCCTGAGGGCTTACAGCAACCTCAA 1380
Qy 461 ValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAsp 480
Db 1381 GTACTGTATCAGAAACAATGATTAATAGCTACATGCTTGGAAACAAGACCACTGGAT 1440
Qy 481 ProGlyThrAlaGlyProArgValTrpTyrArgProIleProSerHisMetProSerLeu 500
Db 1441 CCAGGAAACAGAGGCTCCAGAGTTGTGTAAGGCCAATTCGAATCATATGCTAGTCTG 1500
Qy 501 HisAsnIleProValProGluThrAspTyrLeuGluAsnThrProThrMetProPheSer 520
Db 1501 CATATATATCCAGTCTGAGACCACTATCTAGGAAATATACCCACCATGCACTTACGC 1560
Qy 521 SerLeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGln 540
Db 1561 TCCTTGCACCAACAGATGATCTATAAATATATACATATACAAATAGTACGCTTCAG 1620
Qy 541 IleGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThr 560
Db 1621 ATTGAGCCTTCAATTAATATGAGATGTGTGGAGAGCTTCACTACTAGACAGCAC 1680

QY 561 AsnThrAsnPhleuSgluProAlaAlaIalysTyrGlnAlaIlePheAspAsnThrThr 580
DB 1681 AATACGAGCTTCAAGAGAGAGCCAGCTAGTACCAAGCTATCTTGATTAATACCACT 1740
QY 561 SerLeuThrAspLysHisLeuAspProIleArgIuAsnLeuGlyLysHisTyrLysAsn 600
DB 1741 AGCTGACGAGTAACACCTGACCCCAATCGAGAAATCTGGGAACACACTGGAAAC 1800
QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGlu 620
DB 1801 TGTGCCCGTAACCTGGGCTTCACACAGTCTCAGATTGATGAATGACCATGACATATGAG 1860
QY 621 ArgAspGlyLeuLysGlyLysValTyrGlnMetLeuGlnLysTyrValMetArgGluGly 640
DB 1861 CGAGATGAGACTGAAAGAAAGGTTTACAGATGCTCAAAAGTGGGTGATGAGGAGAGGC 1920
QY 641 IleLysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgTlleAsp 660
DB 1921 ATAAAGGAGCCACCGGTGGGAGAGCTGCCCGCCGCTCCACCAAGTGTTCAGAGATCCAG 1980
QY 661 LeuLeuSerSerLeuIleTyrValSerGlnAsn 671
DB 1981 CTTCTGACGAGCTTGATTACCTCAGCCAGAAC 2013
RESULT 7
AAT43753
ID AAT43753 standard; cDNA: 2137 BP.
AC AAT43753;
XX
DT 13-FEB-1997 (first entry)
XX
DE Human receptor interacting protein gene.
XX
KW Receptor interacting protein; RIP; cell death; apoptosis;
KM Fas; Apo-1; signal transduction; cancer; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2016
FT /tag= a
XX
PN WO9636730-A1.
XX
PD 21-NOV-1996.
XX
PF 18-APR-1996; 96WO-US05386.
XX
PR 18-MAY-1995; 95US-0444005.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (HARD) HARVARD COLLEGE.
XX
PI Kim E, Leder P, Lee T, Seed B, Stranger BZ;
XX
DR MPI: 1997-012100/01.
DR P-PSDB; AAM04628.
XX
PT Receptor interacting protein having death and kinase domain - useful
PT to control diseases that involve abnormal apoptosis, and for
PT diagnosis and drug screening
XX
PS Disclosure: Page 42-43; 64pp. English.
XX
CC A DNA sequence (AAT43753) codes for human receptor interacting protein
CC (RIP) (AAM04628), a protein that contains a C-terminal death domain
CC through which RIP interacts with the Fas/Apo-1 intracellular domain
CC (ICD). RIP overexpression leads to cell death. The RIP DNA was
CC identified in a yeast two-hybrid screen of a human T-cell cDNA
CC library for proteins that interacted with the Fas/Apo-1 ICD, and by
CC screening a cDNA library with murine RIP cDNA (AAT43752). It can be

CC used as a probe, to produce recombinant RIP in host cells, and in
CC gene therapy either to control the number of cells bearing a
CC specific gene, or to act as an antitumor agent in forms of cancer
CC therapy dependent on delivery of a lethal gene to neoplastic cells.
XX
SQ Sequence 2137 BP; 658 A; 472 C; 550 G; 457 T; 0 other;
Alignment Scores:
Pred. No.: 1,33e-261 Length: 2137
Score: 3513.00 Matches: 666
Percent Similarity: 99.40% Conservative: 1
Best Local Similarity: 99.25% Mismatches: 4
Query Match: 99.10% Indels: 0
DB: 18 Gaps: 0
US-09-981-397a-16 (1-671) x AAT43753 (1-2137)
QY 1 MetGlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGluSer 20
DB 1 ATGCACACGACATGCTCTTCAATGATCATTAAGATGAATCCAGTGAAGTCTGACAGAGT 60
QY 21 AlaGluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyCysPheHisArgThrGlnGly 40
DB 61 GCAGAACTGAGACGCGGAGGCTTCGCGAAGGTCTCTGTCTTCCACAGAACCCAGAGGA 120
QY 41 LeuMetIleMetLysThrValTyrLysGlyProAsnCysIleGluHisAsnGluAlaLeu 60
DB 121 CTCATGATCATGAATAACAGTGTACAGGGGCCCACTGATTTGAGCACACAGAGCCCTC 180
QY 61 LeuGluGluAlaLysMetMetLeuAsnArgLeuArgHisSerArgValValLysLeuLeuGly 80
DB 181 TTGAGAGAGCGGAGATGATGATGACAGACTGACACACACCGGCGTGGAACCTCTCTGGGC 240
QY 81 ValIleIleGluGluGlyLysTyrSerLeuValMetGluTyrMetGluLysGlyAsnLeu 100
DB 241 GTCATCATGAGAGGAGGAGAGTACTCCTGCTGATGAGAGTACATGAGAGAGGACACCTG 300
QY 101 MetHisValLeuLysAlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
DB 301 ATGCACGTGCTGAAGCCGAGATGAGTACTCGCTTCTGTAAAGAGAGATATTTTG 360
QY 121 GluIleIleGluGluGlyMetCysTyrIleuHisGlyLysGlyValIleHisLysAspLeuLys 140
DB 361 GAATCATTTGAAGCATGCTCTACTTACATGAAAGCGCTGATACCAAGACCTTGAG 420
QY 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAla 160
DB 421 CCGTAATATTCCTTGTTGATTAATGACTTCCACATTAAGATCGAGACCTGGCCTTGCC 480
QY 161 SerPheLysMetIlePheSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAsp 180
DB 481 TCCTTTAAGATGTGAGCAACCTGATTAATGAGCAATGAGCTGAGGAGAGTGCAG 540
QY 181 GlyThrAlaLysLysAsnGlyGlyLysThrLeuTyrTyrMetAlaIleProGluHisLeuAsnAsp 200
DB 541 GGCACCGCTTAAGAAAGATGGCGGCACCTCTACTACATGAGGCGCCGAGACCTTAATGAC 600
QY 201 ValAsnAlaLysProThrGluLysSerAspValTyrSerPheAlaValIleLeuTyrAla 220
DB 601 GTCAACGCAAGCCCAACAGAGAGAGTGGATGTGACACTTTGCTGTAGTACTGGGCG 660
QY 221 IlePheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnGluLeuIleMetCys 240
DB 661 AATATTGCAAATAGAGAGCATATGAATGCTATCTGTGAGCAGACATGATATATGTC 720
QY 241 IleLysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIle 260
DB 721 ATTAATATCGGGAACAGGCGACATGTGATGATGATGATGATGATGATGATGATGATGAT 780
QY 261 IleSerLeuMetLysLeuGlyTyrGluAlaAsnProGluAlaArgProThrPheProGly 280
DB 781 ATCAGTCTCATGAACTCTGCTGGGAGAGCAATCCGGAAGCTGGCGCACATTTCTGCGC 840

QY 281 ILeGluGluYusPhearProPheTYrLeuSerGlnLeuGluGluSerValGluGluAsp 300
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 Db 841 ATTAGAAGAGAAAAATTAGCCCTTTTATTATTAGTCAATTAGAGAAAGTGTAGAGAGAGAC 900
 QY 301 ValIysSerLeuYusGluTYrSerAsnGluAsnAlaValValIysArgMetGluSer 320
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 Db 901 GTGAAGAGTTTAAAGAAAGAGATTCAACAGAAATCAGTGTGAGAGAAATCAGACT 960
 QY 321 LeuGlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGluGlnPro 340
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 Db 961 CTTCAACTGATATTGTGGCAGTACTTCAAGCCGGTCAATTTAGCCACAGAACAGAGCT 1020
 QY 341 GlySerLeuHisSerSerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAla 360
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 Db 1021 GGTTCACTGCACAGATCTCCAGGAGCTTGGATGGGTCTGTGGAGAGTCTGTGTTGGT 1080
 QY 361 ProSerLeuGluHisProGlnGluGluAsnGluProSerLeuGlnSerLysLeuGluAsp 380
 |||||||
 Db 1081 CCTCCCTGGAGACCAACCAAGAAAGAAATGAGCCCGCCAGACTTAAACTCCAGAC 1140
 QY 381 GluAlaAsnTYrHisLeuTYrGlySerArgMetAspArgGlnThrLysGlnGlnProArg 400
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 Db 1141 GAAGCCCACTACCTTTATTAGCAGCCGATGGACAGGACAGAGAAACAGACCCAGAC 1200
 QY 401 GlnAsnValAlaTYrAsnArgGluGluGluAlaArgArgArgValSerHisAspProPhe 420
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 Db 1201 CAGATATGGCTTTCACACAGAGAGAGAGAAAGAGAGAGCGAGGCTCTCCATGACCTTTT 1260
 QY 421 AlaGlnGlnArgProTYrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTYrSer 440
 |||||||
 Db 1261 GCACAGCAAGACCTTACGAGAAATTTTCAGAAATACAGAGGAAAGGACACTGTTTATTC 1320
 QY 441 SerAlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGln 460
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 Db 1321 AGTCACAGCCAGTCATGTAATGACGTCCACCAATACAGGCTCCACAGCAACCTCAA 1380
 QY 461 ValLeuTYrGlnAsnAsnGlyLeuTYrSerSerHisGlyPheGlyThrArgProLeuAsp 480
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 Db 1381 GFACTGTATCAGAAACATGGATTATATAGCTCACATGGCTTGTGACACAGACCTGGAT 1440
 QY 481 ProGlyThrAlaGlyProArgValTYrTYrArgProIleProSerHisMetProSerLeu 500
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 Db 1441 CCAGGACACAGAGCTCCACAGATTGGTACAGGCCAATTCACATGATATGCCATGCTG 1500
 QY 501 HisAsnIleProValProGluTYrAsnTYrLeuGlyAsnThrProThrMetProPheSer 520
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 Db 1501 CATTAATATCCAGAGCTGAGACCACTATCTAGGAATTCCTCCACATGCCATTCAGC 1560
 QY 521 SerLeuProProThrAspGluSerIleLysTYrThrIleTYrAsnSerThrGlyIleGln 540
 |||||||
 Db 1561 TCCTGGCCACACAGATGATCTATTAATATATACATATACATAGTACTGGCATTCAG 1620
 QY 541 IleGlyAlaTYrAsnTYrMetGluIleGlyLysThrSerSerSerLeuLeuAspSerThr 560
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 Db 1621 ATTAGAGACCTACAAATATATGAGATGTTGGTGGACGAGTTCACTACACTAGACAGACA 1680
 QY 561 AsnThrAsnPheLysGluGluProAlaAlaLysTYrGlnAlaIlePheAspAsnThrThr 580
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 Db 1681 AATAAGCAACTTCAAAAGAGAGCCAGCTGAAGTACACAGCTATCTTGAATAATCCACT 1740
 QY 581 SerLeuThrAspLysHisLysAspProIleArgGluAsnLeuGlyLysHisTrpLysAsn 600
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 Db 1741 AGTCTGACGATTAACACCTGGACCCCAATCAGGAAAAATCTGGAAAAAGCAGCTGAAAAAC 1800
 QY 601 CysAlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTYrGlu 620
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 Db 1801 TGTGCCCGTAAACGTGCGCTTCACACAGCTCAGATGATGAATAATGCACATGACTATGAG 1860
 QY 621 ArgAspLysLeuYusGluYusValTYrGlnMetLeuGlnLysTrpValMetArgGluGly 640
 |||||||
 Db 1861 CGGATGAGACTGAAAGAAAGGTTTACCAATGCTTCCAAAAGTGGGATGATGAGGAAGGC 1920
 QY 641 IleYusGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAsp 660

Db 1921 ATAAAGGAGCCAGCGGGGGAAGCTGCGCCAGGCGCTCCACAGCTGTCCAGGATGCGAC 1980
 QY 661 LeuLeuSerLeuIleTYrValSerGlnAsn 671
 |||||||
 Db 1981 CTTCTGAGCAGCTTGATTTACGTACGACGAGAAC 2013
 RESULT 8
 AAS13810
 ID AAS13810 standard; DNA: 9687 BP.
 XX
 AC AAS13810;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE DNA encoding shuttle vector pPYC.
 DE
 KW Shuttle vector; pPYC; circular; cyclic; yeast transformation: ds.
 KW
 XX
 OS Synthetic.
 XX
 FH Location/Qualifiers
 FH 1..750
 FH promoter
 FT
 FT /tag= a
 FT /note= "Cytomegalovirus (CMV) promoter"
 FT 1158..1662
 FT misc_feature
 FT
 FT /tag= b
 FT /product= "IRES"
 FT /note= "Internal ribosome entry sequence"
 FT 1683..2402
 FT CDS
 FT
 FT /tag= c
 FT /product= "GFP"
 FT /note= "Green fluorescent protein"
 FT 2985..4332
 FT misc_feature
 FT
 FT /tag= d
 FT /note= "Yeast 2 mu origin of replication"
 FT 4868..5542
 FT CDS
 FT
 FT /tag= e
 FT /product= "TRP"
 FT /note= "Tryptophan"
 FT 5982..6842
 FT CDS
 FT
 FT /tag= f
 FT /product= "Beta lactamase"
 FT /note= "Ampicillin resistance"
 FT 7142..7669
 FT misc_feature
 FT
 FT /tag= g
 FT /note= "E. coli origin of replication"
 FT
 PN US6280937-B1.
 XX
 XX 28-AUG-2001.
 PD
 XX
 XX 14-AUG-1998; 98US-0133944.
 PF
 XX
 XX 14-AUG-1998; 98US-0133944.
 PR
 XX
 XX (RIGE-) RIGEL PHARM INC.
 PA
 XX
 XX Luo Y, Yu PW, Lorens J;
 XX
 XX WPI: 2001-588953/66.
 DR
 XX
 XX Screening for a nucleic acid producing a preferred activity or
 FT phenotype in a mammalian cell by transforming yeast with shuttle vector
 FT having an origin of replication, selectable gene, promoter and
 FT homologous recombination site
 FT
 PS Disclosure: Fig 5; 40pp: English.
 XX
 XX The invention relates to a method of screening for a nucleic acid that
 CC produces a preferred activity or phenotype in a mammalian cell comprising
 CC transforming yeast with a shuttle vector. An advantage of the yeast
 CC system is its efficiency at homologous recombination, and eliminates the

CC steps of manipulating the ends of the vector and the heterologous nucleic acid and ligating the two together. Another advantage is that the yeast CC can be transformed with large nucleic acids, i.e. up to at least 10 kb, CC which can then be inserted into the vector. The present sequence CC represents the coding sequence of shuttle vector pYC used in the CC method of the invention.

XX Sequence 9687 BP; 2643 A; 2220 C; 2370 G; 2454 T; 0 other;

Alignment Scores:

Pred. No.:	3,9e-260	Length:	9687
Score:	3505.00	Matches:	668
Percent Similarity:	99.70%	Conservative:	0
Best Local Similarity:	99.70%	Mismatches:	2
Query Match:	98.87%	Indels:	1
DB:	22	Gaps:	0

US-09-981-397a-16 (1-671) x AAS13810 (1-9687)

QY 2 GlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSerAla 21
DB 1134 CACACAGACATGCTCTTGAATGTCATTAAAGATGAATCCAGTACTTCTGGAGAGTGA 1193
QY 22 GluLeuAspSerGlyGlyPheGlyLysValSerLeuGlyPheHisArgThrGlnGlyLeu 41
DB 1194 GAACGTGACAGCGGAGGCTTTGGGAAGGTGTCTGTCTGTTCCACAGAACCCAGGAGACTC 1253
QY 42 MetIleMetLysThrValTyrLysGlyProAsnGlyIleGlnHisAsnGlnAlaLeu 61
DB 1254 ATGATCATGAATAACAGTGTACAGAGGCGCCCACTCATTTGACACACAGAGGCGCTCTTG 1313
QY 62 GlnGlnAlaLysMetMetLeuAsnArgLeuArgHisSerArgValValLysLeuGlnLysAl 81
DB 1314 GAGGAGCGGAGATGATGATGACAGACTGAGACACAGCCGGGTGTAAGTCTCTGGGCGTC 1373
QY 82 IleIleGlnGlnGlyLysTyrSerLeuValMetGluTyrMetGlnLysGlyAsnLeuMet 101
DB 1374 ATCATAGAGAGAGGAGAGTACTCCCTGGATGAGATGATGGAAGGCGCAACTGTATG 1433
QY 102 HisValLeuLysAlaIleGlnMetSerThrProLeuSerValLysGlyArgIleIleGln 121
DB 1434 CACGTGCTGMAAGCCGAGATGACTCCGCTTCTGTAAAGAGAAAGTAAATTGGGAA 1493
QY 122 IleIleGlnGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysPro 141
DB 1494 ATCATTTGAAGGAATGTGCTACTTACATGA -AAGGCGGATACACAGAGACTGAAGCT 1552
QY 142 GluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSer 161
DB 1553 GAAATATATCTTGTGATTAATGACTTCCACATTAAAGATCGCAGACCTCGGCTTCCTCC 1612
QY 162 PheLysMetTyrSerLysLeuAsnAsnGlnGluHisAsnGluLeuArgGluValAspGly 181
DB 1613 TTTAAGATGTGACGAACACTGAATATGAGAGCCCAATGACTGAGGAAATGGAGGCG 1672
QY 182 ThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaProGlnHisLeuAsnAspVal 201
DB 1673 ACCGCTAAGAAAGATGCGCGCCCTTACTACTATGCGCCCGAGACCTGAATGAGCGTC 1732
QY 202 AsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValValLeuTyrAlaIle 221
DB 1733 AACGGAAGCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1792
QY 222 PheAlaAsnLysGlnProTyrGlnAsnAlaIleCysGlnGlnGlnLeuIleMetCysIle 241
DB 1793 TTTCGAATTAAGACCATATGAAATGCTATCTGTGACAGCAGACTGTGATTAATGTGCATA 1852
QY 242 LysSerGlyAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIleIle 261
DB 1853 AATCTGGGAACAGCGCATGTGATGATGATGATGATGATGATGATGATGATGATGATG 1912
QY 262 SerLeuMetLysLeuGlyTyrGlnAlaAsnProGlnAlaArgProThrPheProGlyIle 281
DB 1912

DB 1913 ACTCATGAGACTCTGCTGGGAAGCGAATCCGAGAGCTCGCGACATTTCTTGCGCAT 1972
QY 282 GlnGluLysPheAsnArgProPheTyrLeuSerGlnLeuGlnIleValGlnLysAspVal 301
DB 1973 GAGAGAAATTTAGGCTTTTATTTAATTAAGTAAATTAAGAAAGTGAAGAGAGAGCTG 2032
QY 302 LysSerLeuLysLysGlnTyrSerAsnGlnAsnAlaValValLysArgMetGlnSerLeu 321
DB 2033 AAGACTTTAAAGAAAGACTATTTCAACAGAAATGAGTGTGAGAGAGATGACTCTCTT 2092
QY 322 GlnLeuAspCysValAlaValProSerSerArgSerAsnSerAlaThrGlnLysProGly 341
DB 2213 TCCTCGAGACACCCCAAGAGAGATGAGCCAGCCGACAGATTAATCCAGAGAGCA 2272
QY 382 AlaAsnTyrHisLeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGln 401
DB 2273 GCCAACTACCATCTTTATGGAGCGCGCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2332
QY 402 AsnValAlaTyrAsnArgGlnGlnGlnArgArgArgValSerHisAspProPheAla 421
DB 2333 AATGTGCTTACACAG 2392
QY 422 GlnGlnArgProTyrGlnAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSerSer 441
DB 2393 CAGCAAAAGACCTTACAGAAATTTTCAAGATACAGAGGAGAGAGAGAGAGAGAGAGAG 2452
QY 442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal 461
DB 2453 GCAGCAGCTCATGTAAGTGCAGTGCAGAGCCCTCAGGCTCAGGAGAGAGAGAGAGAG 2512
QY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
DB 2513 CTGTATCAGAACATAGATTAATATAGCTCAGATGCTTGGAGAGAGAGAGAGAGAGAGAG 2572
QY 482 GlyThrAlaGlyProArgValTyrPyrArgProIleProSerHisMetProSerLeuHis 501
DB 2573 GGAACAGAGAGGCGCAGAGATTTGGTACAGGCCAATTCAGATCATCTGATGCTGAT 2632
QY 502 AsnIleProValProGlnThrAsnTyrLeuGlnLysAsnThrProThrMetProPheSerSer 521
DB 2633 AATATCCAGATGCTGAGACCAACATATCTAGAAATACACCCACCATGCTCAGCTCC 2692
QY 522 LeuProProThrAspGlnSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIle 541
DB 2693 TTGCCACCAACAGATGATCTATAATATATACATATATACATATATATATATATATAT 2752
QY 542 GlyAlaTyrAsnTyrMetGlnIleGlyLysThrSerSerSerLeuLeuAspSerThrAsn 561
DB 2753 GGAGCCTCAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2812
QY 562 ThrAsnPheLysGlnGlnProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer 581
DB 2813 ACGAACTTCAAG 2872
QY 582 LeuThrAspLysHisLeuAspProIleArgGlnAsnLeuGlyLysHisTyrLysAsnGly 601
DB 2873 CTGACGAGATTAACACTGAGACCATATCAGGAGAAATCTGGGAGAGAGAGAGAGAGAG 2932
QY 602 AlaArgLysLeuGlyPheThrGlnSerGlnIleAspGlnIleAspHisAspTyrGlnArg 621
DB 2933 GCCCGTAAACTGCGCTTCACACAGCTCAGATTCAGATTCAGATTCAGATTCAGATTCAG 2992
QY 622 AspGlyLeuLysGlnLysValTyrGlnMetLeuGlnLysTyrPheValMetArgGlnGlyIle 641
DB 2993 GATGAGCTGAAAG 3052

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OY 642 LysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAspLeu 661
DB 3053 AAGGAGCAGCGTGGGAGACGTGCCAGCGCTCCACAGATGTTCCAGATCAGCTT 3112
OY 662 LeuSerSerLeuIleTyrValSerGlnAsn 671
DB 3113 CTGAGCAGCTTGATTTACGTACGACGAGAAC 3142

RESULT 9
ABK15129
ID ABK15129 standard; DNA; 9687 BP.
AC ABK15129;
XX 08-MAY-2002 (first entry)
DE Plasmid pPYC.
XX Plasmid pPYC; transformation; homologous recombination;
KW cyclic; ds.
OS Synthetic.
XX Key Location/Qualifiers
FH 1..750
FT promoter
FT /tag= a
FT /label= CMV
FT /note= "Cytomegalovirus"
FT 1158..1662
FT /tag= b
FT /label= IRES
FT /note= "Internal ribosome entry site"
FT 1683..2402
FT /tag= c
FT /product= "GFP"
FT /note= "Green fluorescent protein"
FT 2985..4332
FT /tag= d
FT /label= yeast_2micron
FT 4868..5542
FT /tag= e
FT /product= "TRP"
FT /note= "Tryptophan synthesis gene"
FT 5982..6842
FT /tag= f
FT /product= "Amp resistance gene"
FT /note= "Ampicillin"
FT 7142..7669
FT /tag= g
FT /note= "Escherichia coli origin of replication"
XX US2002001830-A1.
XX 03-JAN-2002.
XX 09-DEC-1998; 98US-0208827.
XX 14-AUG-1998; 98US-0133944.
XX (LUOY/) LUO Y.
XX (YUFW/) YU P W.
XX (LORE/) LORENS J.
XX Luo Y, Yu PW, Lorens J;
XX MPI, 2002-163702/21.
XX Shuttle vector capable of replication in yeast and expression in
XX mammalian cells, useful for transforming yeast, comprises origin of
XX replication and selectable gene functional in yeast and promoter
XX functional in mammalian cell

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PS Example 2: Fig 5A-D; 54pp; English.
XX The invention describes a shuttle vector comprising an origin of
CC replication functional in yeast, a selectable gene functional in yeast,
CC and a promoter functional in a mammalian cell e.g. HeLa cells and capable
CC of directing transcription of a polypeptide coding sequence operably
CC linked downstream from the promoter. The shuttle vector is used to
CC transform yeast. The heterologous nucleic acids are then introduced to
CC the yeast and homologous recombination takes place such that the yeast
CC inserts the heterologous nucleic acid into the shuttle vector at a
CC specific insertion site i.e. a homologous recombination site. The shuttle
CC vectors are then isolated from the yeast and used to transform mammalian
CC cells for expression of the heterologous nucleic acid. The shuttle vector
CC allows exploitation of the yeast two-hybrid system and homologous
CC recombination, and also provides expression in mammalian cells to verify
CC protein-protein interactions, and to study proteins function. This
CC sequence represents the plasmid pPYC, described in the method of the
CC invention.
XX
SQ Sequence 9687 BP; 2643 A; 2220 C; 2370 G; 2454 T; 0 other:

Alignment Scores:
Pred. No.: 3.9e-260 Length: 9687
Score: 3505.00 Matches: 668
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 2
Query Match: 98.87% Indels: 1
DB: 24 Gaps: 0

US-09-981-397A-16 (1-671) x ABK15129 (1-9687)

OY 2. GlnProAspMetSerLeuAsnValIleLysMetLysSerSerAspPheLeuGlnSerAla 21
DB 1134 CAACGACACATGCTCTGATGTCAATTAGAGAAATCCAGAGCTTCTCGAGAGTGCA 1193
OY 22 GluLeuAspSerGlyGlyPheGlyLysValSerLeuCysPheHisArgThrGlnIleu 41
DB 1194 GAACGTGACAGCGGAGGCGCTTGGAGAGGTCTGCTGTGTTCCACAGAACCCAGGAGAC 1253
OY 42 MetIleMetLysThrValTyrIleLysGlyProAsnCysIleGlnHisAsnGlnAlaLeu 61
DB 1254 ATGATCATGAAACAGAGTGTACAGAGGCCCACTCATGTGACACACAGGCCCTCTTG 1313
OY 62 GlnGluAlaLysMetLeuAsnArgLeuArgHisSerArgValValLysLeuGlnVal 81
DB 1314 GAGGAGCGAAGATATGATGACAGACTGACACACACCGGTGTGTAAAGCTCTCGGCGTC 1373
OY 82 IleIleGlnGlnGlyLysTyrSerLeuValMetGluTyrMetGluLysGlnLysLeuMet 101
DB 1374 ATCATAGAGGAGGAGAGTACCTCGGTGATGAGATCATGTGAGAGGCAACCTGATG 1433
OY 102 HisValLeuLysAlaGlnMetSerThrProLeuSerValLysGlyArgIleLeuGln 121
DB 1434 CACGTGCTGAAAGCCGAGATGAGTACTCGCTTCTGTAAAGGATTAATTTGGGAA 1493
OY 122 IleIleGlnGlnMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLysPro 141
DB 1494 ATCATTTGAGGAGATGCTACTTACATGA- AAGGCGTGATACACAGACCTGAAGCCT 1552
OY 142 GluAsnIleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlnLysLeuAsp 161
DB 1553 GAAATATTCCTTGTTGATATATGACTTCCACATTAAAGATCGAGACCTGCTTCCTCC 1612
OY 162 PheLysMetTrpSerLysLeuAsnGlnGlnHisAsnGlnLysLeuArgGlnValAspGly 181
DB 1613 TTTAAGATGTGAGCAACTGAAATATGAGAGCAACATGAGCTGAGGGAATGTGAGCGCC 1672
OY 182 ThrAlaLysLysAsnGlyLysThrLeuTyrTyrMetAlaProGlnHisLeuAsnSpsVal 201
DB 1673 ACCGCTAAGACAAATGGCGGACCTCTTACTACATGCGGCCGAGACCTGATATACGTC 1732
OY 202 AsnAlaLysProThrGlnLysSerAspValTyrSerPheAlaValLeuTrpAlaIle 221

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Db 1733 AACGCAAGCCACAGAGAGATGATGTGTACAGCTTTCTGTAGTACTGTGGGATA 1792
 QY 222 PheAlaAsnLysGluProTyrGluAsnAlaIleCysGluGlnIleuIleMetCysIle 241
 Db 1793 TTGGCAATATAGAGAGCCATATGAATGCTATCTGTGACGACAGATTGATTAATGTGATA 1852
 QY 242 LysSerGluAsnArgProAspValAspAspIleThrGluTyrCysProArgGluIleIle 261
 Db 1853 AAATCTGGAGAACAGCCAGATGTGATGACATCAGTACAGTACGCCAAGAAATATATC 1912
 QY 262 SerLeuMetLysLeuCysTrpGluAlaAsnProGluAlaArgProThrPheProGlyIle 281
 Db 1913 AGTCTGATGAAGCTCTGCTGGAGGCAATCCGGAAGCTCGCCGACATTTCTGTGCATT 1972
 QY 282 GluGluLysPheArgProPheTyrLeuSerGlnLeuGlnIleuSerValGlnIleAspVal 301
 Db 1973 GAAGAAATTTAGGCTTTTATTTAAGTCATTTGAAGAAGTGTAGAGAGACGTG 2032
 QY 302 LysSerLeuLysLysGluTyrSerAsnGluAsnAlaValLysArgMetGlnSerLeu 321
 Db 2033 AAGAGTTTAAAGAAAGATATTCAAACGAAATGCAAGTTGTGAAGCAATGCAGTCTCT 2092
 QY 322 GlnLeuAspCysValAlaValProSerSerArgSerAsnSerLeuThrGlnIleProGly 341
 Db 2093 CAATCTGATTTGTGTGGCAGTACCTTCAGCCGGTCAAAATTCACCCACAGACAGCTGTG 2152
 QY 342 SerLeuHisSerSerGlnGlnIleuGlyMetGlyProValGlnIleuSerTrpPheAlaPro 361
 Db 2153 TCATCTGACAGATTCCCGAGGAGACTTGGGATGGTCTCTGTGAGAGATCTCTGTTCCT 2212
 QY 362 SerLeuGlnHisProGlnIleuGluAsnGluProSerLeuGlnSerLysLeuGlnAspGlu 381
 Db 2213 TCCTGTGAGCACCACAGAAAGAGAAATGAGACCCAGCTCGAGATGAACCTCCAAAGCAA 2272
 QY 382 AlaAsnTyrHisLeuTyrGlnSerArgMetAspArgGlnThrLysGlnIleProArgGln 401
 Db 2273 GCCAATCACCATTCTTATGTGACGCCCATGTGACAGCAGCAGAAACGCCACAGACAG 2332
 QY 402 AsnValAlaTyrAsnArgGlnIleuGluArgArgArgValSerHisAspProPheAla 421
 Db 2333 AATGTGCTTACAAACAGAGAGAGAAAGAGAGAGCGGTCTCCCATGACCTTTTGCA 2392
 QY 422 GlnGlnArgProTyrGluAsnPheGlnAsnThrGlnGlyLysGlyThrValTyrSerSer 441
 Db 2393 CACCAAGACCTTACGAGAAATTTTCAGAAATACAGAGGAAAGCACTGTTTATTCAGT 2452
 QY 442 AlaAlaSerHisGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnVal 461
 Db 2453 GCAGCCAGTCATGTATGATGACAGTGCACACACCCCTCAGGGCTCAGACCCACCTCAAGT 2512
 QY 462 LeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspPro 481
 Db 2513 CTGTATACAGAAATGATATATATAGTCTCATGTGGCTTGTGACAGACACATGGATCCA 2572
 QY 482 GlyThrAlaGlyProArgValTrrPyrArgProIleProSerHisMetProSerLeuHis 501
 Db 2573 GGAACAGCAGCTCCAGAGTTGTGACAGGCCAAATTCAGATCATATGCTTACTGTGCAT 2632
 QY 502 AsnIleProValProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSer 521
 Db 2633 AATATCCCACTGCTGAGACCACTATCTAGAAATACACCCACCATGCATTCAGCTCC 2692
 QY 522 LeuProProThrAspGluSerIleLysTyrThrIleTyrAsnSerThrGlyIleGlnIle 541
 Db 2693 TTGCCACCAACACATGATATATAATATATACATATACAAATAGTACTGCAATTCAGATT 2752
 QY 542 GlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSerSerLeuLeuAspSerThrAsn 561
 Db 2753 GGAGCTTACATATATATGAGATTGGTGGACGAGTTCACTACTAGCACACCAAAAT 2812
 QY 562 ThrAsnPheLysGlnIleProAlaAlaLysTyrGlnAlaIlePheAspAsnThrThrSer 581
 Db 2813 ACGAATCTCAAAAGAGCAGCTGCTAGTACCAACGATATCTTTGATATATACACTAGT 2872

QY 582 LeuThrAspLysHisLeuAspProIleArgGluAsnLeuGlyLysHisTrpLysAsnCys 601
 Db 2873 CTGACGATATACACCTGACCAATTCAGAGAAATCTGGAAAGACACTGGAAAACTGT 2932
 QY 602 AlaArgLysLeuGlyPheThrGlnSerGlnIleAspGluIleAspHisAspTyrGluArg 621
 Db 2933 GCCCTTAACATGGCGCTTCCACACAGTCTCAGATTGATGAATATGACCATGACTATGAGCGA 2992
 QY 622 AspGlyLeuLysGluLysValTyrGlnMetLeuGlnLysTrpValMetArgGluGlyIle 641
 Db 2993 GATGGACTGAAAGAAAGTTTACAGATGCTCCAAAGTGGGTGATGAGGAGAGGCATA 3052
 QY 642 LysGlyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIleAspLeu 661
 Db 3053 AAGGAGCCACGGTGGGAAAGCTGGCCAGGGGCTCCACAGATGTTCCAGATTCAGACTT 3112
 QY 662 LeuSerSerLeuIleTyrValSerGlnAsn 671
 Db 3113 CTGAGCAGCTGTGATTTACCTCACCCAGAAC 3142
 RESULT 10
 ID AAV99818 standard; cDNA; 3750 BP.
 AC AAV99818;
 XX 12-APR-1999 (first entry)
 DT
 DE Human receptor interacting factor RIP cDNA.
 XX
 KW Receptor interacting protein; RIP; RIP-interacting factor; RIF;
 KW human; apoptosis; ds.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 52..2022
 FT /*tag= a
 PN WO9857985-A2.
 XX
 PD 23-DEC-1998.
 XX
 PF 19-JUN-1998; 98MO-US12778.
 XX
 PR 19-JUN-1997; 97US-0050196.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Shaoon B;
 XX
 DR WPI: 1999-095325/08.
 XX
 PT P-PSDB; AAW80994.
 XX
 PS New human RIP-interacting factor - used e.g. to treat muscle
 XX wasting diseases and autoimmune diseases
 XX
 PS Disclosure; Page 42-44; 57pp; English.
 XX
 CC This is the nucleotide sequence of cDNA encoding human receptor
 CC interacting protein (RIP, see AAW80994), a protein involved in the
 CC Fas-mediated cell death pathway. The invention relates to a novel
 CC human RIP interacting factor, RIF (see AAW80993) that is involved in
 CC the regulation of programmed cell death. RIF cDNA (see AAV98817) was
 CC isolated from a placenta library by two-hybrid analysis with
 CC murine RIP as bait. Modulation of RIF activity can be used to
 CC induce or prevent apoptosis, e.g. for the treatment of cancer,
 CC muscle wasting diseases and autoimmune diseases.
 CC
 SQ Sequence 3750 BP; 1188 A; 822 C; 919 G; 821 T; 0 other;
 Alignment Scores:

OY		400	ArgGlnsAnSVLaLaATyrAsnArGIgUoLnuGrAgtAGrAGrValSerHisASPro	419
Db		1246	AGCGAAATGACGGCTTACACACAGAGAGAGAAAAGAAACCAAGGTCCTCATGACCCC	1305
OY		420	PheAlaGInGlnAarProTyrgLuAsnPheGlnAsnthrGlucylLysGlyThrValTyr	439
Db		1306	TTTGCACAGCAGAGAGCGTCGTGAAGAATATTMAAGAGTGcAGAGACAAGGTCATTGCAT	1365
OY		440	SerSerAlaAlaSerHisSGLyAsnAlaValHisGlnProSerGlyLeuThrSerGlnPro	459
Db		1366	CCCGAGCACAAACGACTCGTGAATTGCCAGTGCACAAAGCTGTCATGCCCCAGCCCAA---	1422
OY		460	GlnValLeuTyrgLnAsnAsnGlyLeuTyrsSerSerHisSGLyPheGlyThrArgProleu	479
Db		1423	-----ACAGTTTGGAACAAATGATTTGTATATATACAGCATGGATTT-----	1461
OY		480	ASPProGlyThraGlaGlyProArgValTrrTyraArProIleProSerHisMetProSer	499
Db		1462	-----GGAGTACAGGTACAGAGAGTGTGGTATCCGCCAAATCTAGCAAAATATAGT	1515
OY		500	LeuHisAsnIleProValProGluThrAsnTyrlEuGlyAsnThrProGHisMetProPhe	519
Db		1516	ACTTATTAATAACTCCAGTCCAGACACCACATACCcGGGAACACACCACCATCCATCCATAC	1575
OY		520	serSerLeuProProthrAspGluSerIleLysTyrrHriLeTyraSerThhGlyIle	539
Db		1576	TTCCTCTGGGCCAGTAGACAGATGACCTCTATAAATATACTATATTCATATAGTTCGTGATTT	1635
OY		540	GlnIleGlyAlaTyraSnTyrmecLuIleGlyLysThrSerSerLeuLeuAspSer	559
Db		1636	CAGATTGGAAACCCAAATTATATATGATGTGTGACATGCAATTC-----CAACCA	1683
OY		560	ThrasnthraSnPhelySGluGluProAlaAlaLysTyrglnAlaIlePheAspAsnthr	579
Db		1684	CCAACAATACTTCCAAAGAAAGAGTCCAGTCCAGACACCAGGCATCTTGTATACACCC	1743
OY		580	ThisSerLeuThraSPryLSHisLeuAsProIleArGGuAsnLeuGlyLysHisTrylps	599
Db		1744	ACTAGTGTGACTGATGAACACACTGAACCTTATCAGGAAAAACCTGGCAAGCAGCATGGAAA	1803
OY		600	AsncysalaArGlysLeuGlyPheThrGlnSerGlnIleaspGluIleasPrhisAspTyr	619
Db		1804	AACGTGTGCCCCCAAGCTGGGCTTCCACTGAGTCTCAGATCGATGAATCGAACCATGACAT	1863
OY		620	GluTrpAspGlyLeuLysGluLysValTyrcImmetLeuGlnLysTrpValMetArgGlu	639
Db		1864	GAAGAGAGTGGACTGAAAGAGAAAGATTACCAAAATGCTTCGAAGTGGCTCATCCGGGAA	1923
OY		640	GlyIleLysSGLyAlaThrValGlyLysLeuAlaGlnAlaLeuHisGlnCysSerArgIle	659
Db		1924	GGCACCAAAAGGGCCACAGTGGGAAGTGGCCACAGCAGACTTCCAAATGTTCGACAGATA	1983
OY		660	AspleuLeuSerSerLeuIleTyrrValSerGlnasn	671
Db		1984	GACCTGCTGAACACTTGATTCGTGGCCAGCCAGAC	2019
RESULT 13				
AASB0491				
ID	AASB0491 standard; cDNA; 2879 BP.			
XX	AASB0491;			
XX	13-FEB-2002 (first entry)			
DE	DNA encoding novel human diagnostic protein #16295.			
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;			
OS	food supplement; medical imaging; diagnostic; genetic disorder; ss.			
PN	WO200175067-A2.			

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|||||
1474 GTCATCATAGAGAGGAGGAGTACTCCCTGGATGGATGATGAGAGAGGACCACTG 1533
Oy MethisValLeuValaGluMetSerThrProLeuSerValLysGlyArgIleIleLeu 120
1534 ATGCACGGTGTGAAGCCGAGATGATGCTCCCTTCTGTAAAGAGATATATTTG 1593
Oy 121 GtutIleIleGluGlyMetCysTyrLeuHisGlyLysGlyValIleHisLysAspLeuLys 140
1594 GAAATCATTTGAAGGAAATGTGCTACTTACATGAAAAGCGTGAATACACAGGACCTGAAG 1653
Oy 141 ProGluAsnIleLeuValAspAsnAspPheHisIleLysIleLeaIle 155
1654 CCTGAAATATCTCTGTGATATATGCTTCCACATTAGATGAGTACTCCGCTTTCTGTA 1713
Oy 155 ----- 155
Db 1714 AAGGAGGATATTTTGGAAATCATTGAAAGATGTGCTACTTACATGAAAAGCGCTG 1773
Oy 156 -----AspLeuGlyLeuAlaSer-----PheLysMet 164
1774 ATACACAGAGCACTGAGCTGAAAATATCTTGTGTATATGACTTCCACATTATAGATG 1833
Oy 165 TTPSerLysLeuAsnGluGluHisAsnGluLeuArgGluValAspGlyThrAlaLys 184
1834 TGGACCAAACTAATATATGAAAGACACATGAGCTGAGGAGAGTGGACGCGCTAG 1893
Oy 185 LysAsnGlyGlyThrLeuTyrTyrMetAlaProGluHisLysAsnAspValAlaLys 204
1894 AAGAATGGCGGACCCCTACTACTACATGGCGCCGAGCACCCTGAATAGCTCAACGCAAG 1953
Oy 205 ProThrGluLysSerAspValTyrSerPheAlaValIleuThrAlaIlePheAlaAsn 224
1954 CCCACGAGAAGTCCGATGTGACAGCTTTCCTGTGATGACTTGGCCATATTTGCCAAT 2013
Oy 225 LysGluProTyrGluAsnAlaIleCysGluGluGlnIleuIleMetCysIleLysSerGly 244
2014 AAGGAGCCATATGAAAATCTATCTGTGAGCAGCATGATATGATATGCAATAAATCTGGG 2073
Oy 245 AsnArgProAspValAspAspIleThrGluTyrCysProArgGluIleIleSerLeuMet 264
2074 AACAGGCCAGATGTGATGACATCACTAGTACTGCCCAAGAAATTTATGAGTCTCATG 2133
Oy 265 LysLeuCysTrpGluAlaAsnProGluAlaArgProThrPhePro----- 279
2134 AACCTGCTGGGAACGAAATCCGGAAGCTCGGCCACATTTCTGTGGTACAAATTCAG 2193
Oy 280 -----GlyIleGluGluLysPheArgProPheTyrIleu 290
2194 AAACACCAAAATGGAAGAGATGTACAAAGCATTTGAAGAAATTTAGGCCCTTTTATTTTA 2253
Oy 291 SerGlnLeuGlnGluSerValGluGluAspValLysSerLeuLysGluLysSerAsn 310
2254 AGTCATTTTGAAGAAAGTGTAGAGAGGACGTGAAGATTTTAAAGGCCCTTACCTCGCGG 2313
Oy 311 GluAsnAlaValAlaLysArgMetGlnSerLeuGlnLeuAspCysValAlaValProSer 330
2314 CACCTAGTAAACCCAGAGCGCTACTCT-----GCCGACCTCGG 2352
Oy 331 SerArg-----SerAsnSerAlaThrGluGlnProGlySerLeuHisSerSerGlnGly 348
2353 AACCGAGAGCGCTACTCCGCCCTCGGAACCCAGACCCCTACTCGCCGACAC--- 2409
Oy 349 LeuGlyMetGlyProValGluGluSerTrpPheAlaProSerLeuGluHisProGlnGlu 368
2410 -----CTCGGAACCCGAGAGCCC-----CTACCTGCGCCA-----CCTCGGAGAC 2448
Oy 369 GluAsnGluProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeuTyrGly 388
2449 CGCAGAGCGCTACCTACCGCCGACCTCGGAACCCAGAGCGCTACCTCGCCGACCTCGGA 2508
Oy 389 SerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArgGlu 408
:::
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Db 2509 ACCGACAGAGCGCTACTGCGGACACTCGGACCGCAGAGCGCTACTGCGGACCTCG 2568
Oy 409 GluGluArgArgArgValSerHisAspProPheAlaGlnIleArgProTyrGluAsn 428
Db 2569 GAACCGAGCGCGCTACTGCGGACCTCGGAGACCGCAGCGGCTACT----- 2619
Oy 429 PheGlnAsnThrGluGluLysGlyThrValTyrSerSerAlaIleSerHisGlyAsnAla 448
Db 2620 -----GCCGACCTCGGAACCGCAGC 2640
Oy 449 ValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeu 468
Db 2641 GCG-----CCTACTGCGCGACCTCGGAACCGCAGCGGCTACTGCGGAC----- 2688
Oy 469 TyrSerSerHisGlyPheGlyThrArg-----ProLeuAspProGlyThrAlaGly 485
Db 2689 -----CTCGGAACCGCAGCGGCTACTGCGGACCTACTGCGGACCTACTGACCGCAGC 2733
Oy 486 -----ProArgValTrpTyrArgProIleProSerHisMet 497
Db 2734 GCGGCTACTGCGCGCAGCTACTGATACCGCAGCGGCTACTGCGG-----CACCTA 2784
Oy 498 ProSerLeuHisAsnIleProValProGluThrAsn 509
Db 2785 GTAAACCGAGAGCGCTACTGCGGACCGCAGCTAGTAAAC 2820
:::
:::
:::

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RESULT 14

AAZ80411
ID AAZ80411 standard; cDNA: 606 BP.

AAZ80411;

07-APR-2000 (first entry)

Human colon cancer cell line SW480 cDNA clone SEQ ID NO:495.

Human; gene expression product; diagnosis; tumour; colon cancer;

colorectal adenocarcinoma; cell line SW480; cell proliferation;

KW cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;

KW hyperplasia; ds.

OS Homo sapiens.

PN WO9664576-A2.

PD 16-DEC-1999.

PF 09-JUN-1999; 99WO-IB01062.

PR 10-JUN-1998; 98US-0088801.

PA (FARB) BAYER CORP.

PI Endge WO, Steimann KE, Astle JH, Burgess CC, Bushnell SE;

PT Carroll E, Catino TJ, Derti A, Ford DM, Lewis ME, Monahan JE;

PI Schlegel R;

PS WPI: 2000-087220/07.

XX Novel nucleic acids, used to develop products for the diagnosis and

PT treatment of disorders involving unwanted cell proliferation,

XX particularly cancers, especially colon cancer

PS Claim 15; Page 328; 469pp; English.

CC AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from

CC the human colorectal adenocarcinoma (colon cancer) cell line SW480. The

CC cDNA clones can be used to generate antisense oligonucleotides which

CC can be used for antisense therapy. Methods and products from the present

CC invention can be used for identifying and/or classifying cancerous cells

CC present in a human tumour, particularly in solid tumours, e.g.

CC carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones

CC can be used for developing agents for the diagnosis and treatment of

CC disorders involving unwanted cell proliferation, such as neoplasia,
CC dysplasia or hyperplasia.

XX Sequence 606 BP; 163 A; 143 C; 158 G; 135 T; 7 other:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score: 521.00	606	99	0
Percent Similarity: 99.00%		Mismatches: 1	
Best Local Similarity: 99.00%		Indels: 0	
Query Match: 14.70%		Gaps: 0	

DB: 21

US-09-981-397a-16 (1-671) x AA280411 (1-606)

```
OY 572 TTYGDLAALAEHSPASNTHTTSSerLeuThrAspLysHisLeuAspProIleArg 591
    |||
DB 3 TACCAAGCTATCTTTGATATACCACTAGCTGACGATTAACACCTGACCAATCAGG 62
    |||
OY 592 GLUAsnLeuGlyLysHisTrpLysAsnCyAlaArgLysLeuGlyPheThrGlnSerGln 611
    |||
DB 63 GAAATCTGGCAAGCACTGCAAAACTGTGCCCTTAACCTGGGCTTCACACACTGCAG 122
    |||
OY 612 ILASPGILLeaspHisAspTyrGluArgAspGlyLeuLysGluLysValTyrGlnMet 631
    |||
DB 123 ATTGATGAATGTGACATGACATGATGAGCGAGATGAGATGAAGAAAGTTTACAGATG 182
    |||
OY 632 LeuGlnLysTrpValMetArgGluGlyIleLysGlyValAlaThrValGlyLysLeuAlaGln 651
    |||
DB 183 CTCCAAAAGTGGTGTGATGAGGAAAGCATTAAGGAGCCAGGCTGGGAAAGCTGGCCAG 242
    |||
OY 652 ALALeuhISGlnCysSerArgIleAspLeuLeuSerSerLeuIleTyrValSerGlnAsn 671
    |||
DB 243 GCGCTCCACAGCTGCTTCGTGATGACCTTCTGACAGCTTCTGACAGCTTATTAACGACGAGAC 302
    |||
```

RESULT 15

AAK94599 ID AAK94599 standard; cDNA; 1871 BP.

XX AAK94599;

XX 06-NOV-2001 (first entry)

XX Human full-length cDNA, SEQ ID NO: 3541.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EP130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-0114089.

XX 08-JUL-1999; 99JP-0194486.

XX 11-JAN-2000; 2000JP-0118774.

XX 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

XX Makamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

XX P-PSDB; AAM93664.

XX 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX Claim 8: SEQ ID NO 3541; 1380BP + sequence listing; English.
XX The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA

CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by

CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping

CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length

CC human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.

XX Sequence 1871 BP; 474 A; 528 C; 516 G; 353 T; 0 other:

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score: 3,47e-26	1871	152	101
Percent Similarity: 461.50%		Mismatches: 187	
Best Local Similarity: 42.59%		Indels: 154	
Query Match: 25.59%		Gaps: 22	

DB: 22

US-09-981-397a-16 (1-671) x AAK94599 (1-1871)

```
OY 1 MetGlnProAspMetSerLeuAsnValIleLys----- 11
    |||
DB 147 CTGGACACCTTCACACCGATGCTGTGCGTCAAGTATGACCCACAGCGTCCCGCCCC 206
    |||
OY 12 MetLysSerSerAspPheLeuGluSerAlaGluLeu---AspSerGlyGlyPheGlyLys 30
    |||
DB 207 TTGGTGTCCATTCAGAGCAACTGAGAGAACACGAGAGCTGTGCGCAAGCGCGGCTCGCACA 266
    |||
OY 31 ValSerLeuGlyPheHisArgThrGlnGlyLeuMetIleMetLysThrValTyrLysGly 50
    |||
DB 267 GTGTTCGGCGGCGCAACATAGCAAGTGGGCGC-----TACGATGTG 305
    |||
OY 51 ProAsnGlyIleGluHisAsnGluAlaLeuLeuGluGluAlaLysMetMetAsnArgLeu 70
    |||
DB 306 GCGGTCAAGATTCGTAACCTGCAAGCGATATCCAGGAGGTCAGAGCCATGCGCAAGCTCG 365
    |||
OY 71 ArgHisSerArgValValLysLeuLeuGlyValIle-----IleGluGlu 85
    |||
DB 366 GATTAACGAATTCGTGCTGCTAGAGGGGTTATCGAAGAGTGAAGTGGACCAAGAT 425
    |||
OY 86 GlyLysTyrSerLeuValMetGluTyrMetGluLysGlyLysLeuMetHisValLeuLys 105
    |||
DB 426 CCCAAGCGCGCTGTGTGACTAAATTCATGAGAACGCGCTCTGTGCGGCTGTGCGAG 485
    |||
OY 106 AlaGluMetSerThrProLeuSerValLysGlyArgIleIleLeuGluIleIleGluGly 125
    |||
DB 486 TCCCAAGTGCCTCGGCGCTGCGCGCTCTTTGGCCGCTGAAAGAAAGTGTGCTTGGG 545
    |||
OY 126 MetCysTyrLeuHisGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 143
    |||
DB 546 ATGTTTAACTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 605
    |||
OY 144 IleLeuValAspAsnAspPheHisIleLysIleAlaAspLeuGlyLeuAlaSerPheLys 163
    |||
DB 606 GTCCTGTGAGCCAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 665
    |||
OY 164 MetTrpSerLysLeuAsnAsnGluGluHisAsnGluLeuArgGluValAspGlyThrAla 183
    |||
DB 666 GGAGGCTACAG-----TCAGGACACGGG 689
    |||
OY 184 Lys---LysAsnGlyLysThrLeuTyrMetAlaProGluHisLeuAsnAspValAsn 202
    |||
DB 690 TCCGGGAGGACGAGGCGACCTGCGCTACTTGGCCCAAGACGTTTGTAAACGTAAC 749
    |||
OY 203 AlaLysProThrGlnLysSerAspValTyrSerPheAlaValIleThrPalaIlePhe 222
    |||
DB 750 CGGAAGGCTCCACAGCAAGTGTACAGCTTTCGGATCTCAATCAATGCGGAGTGTCTT 809
    |||
OY 223 AlaAsnGlyLys-----ProTyrGlu-----AsnAlaIleCysGlu 234
    |||
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Job time : 439 secs

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Db      810 GCTGGAAGAGAGTTGAGTTCACACGAAACATCACTGCTGACAGACAGCTGCACAC 869
QY      235 GlnGlnLeuIleMetCysIleIysSerGlyAsnArgProAspValAspAspIleThrGlu 254
Db      870 AGGCAG-----AACGGCCTTCATGGCTGAGCGCCCA 905
QY      255 TyrCysProArgGlu-----IleIleSerLeuMetLysCysTrpGlu 269
Db      906 GCCGGGCTTACAGACTCCCGGCTTAGAAGAGCTAGAGAGCTAATGCAGCTCTCTGAGC 965
QY      270 AlaAsnProGluAlaArgProThrPhe-----ProGlyIleGluIulysPhe 285
Db      966 AGTGAGCCCAAGACAGACCCCTCTCCAGGAATGCCACCAAAACTGATGAAGCTTC 1025
QY      286 ArgProPheTyrLeuSerGlnLeuGluIulysValGluGluAspValLysSerLeuLys 305
Db      1026 CAG-----ATGTGGAGAACAAATGAAATGCTGCTGCTCCACGGTAAAG 1070
QY      306 LysGluTyrSerAsnGluAsnAlaValIleValysArgMetGlnSerLeuGlnLeuAspCys 325
Db      1071 GATTTCTGCTCTCAGCTCAGACAGACAGCAATAGAGATT----- 1109
QY      326 ValAlaValProSerSerArgSerAsnSerAlaThrGluGlnProGlySerLeuHisSer 345
Db      1110 ---TCTATCCAGAGTCA----- 1124
QY      346 SerGlnGlyLeuGlyMetGlyProValGluGluSerTrpPheAlaProSerLeuGluHis 365
Db      1125 -----GCCCAAGAGGAGACAAATGATGCTTTAGGAGAACCATAGAAAAC 1172
QY      366 ProGlnGluIulysAsnGluProSerLeuGlnSerLysLeuGlnAspGluAlaAsnTyrHis 385
Db      1173 CAGCACTCTGTATGATGTCATGATGTTCTGAGCTGCTA----- 1211
QY      386 LeuTyrGlySerArgMetAspArgGlnThrLysGlnGlnProArgGlnAsnValAlaTyr 405
Db      1212 -----AACAACTGAATCTAGAGAGCTCCAGCTCTGTT----- 1247
QY      406 AsnArgGluGluIulysArgArgValSerHisAspProPheAlaGlnGlnArgPro 425
Db      1248 -----CTAATAAAATGCCCGAGCCT 1268
QY      426 TyrGluAsnPheGlnAsnThrGluGlyLysGlyThrValTyrSer-SerAlaAlaSerHis 445
Db      1269 TACCACAGAGGAGGAGGACAAAGAGAGGCTTCACAGCCCTGGACACAGCACATC 1328
QY      445 sGlyAsnAlaValHisGlnProSerGlyLeuThrSerGlnProGlnValLeuTyrGlnAs 465
Db      1329 TTCAGATTTCATGCCCCAACCT-----CCCCAGACTCCAGAGACCTCAACTTTCAG 1379
QY      465 nasnglyLeuTyrSerSerHisGlyPheGlyThrArgProLeuAspProGlyThrAlaG 485
Db      1380 AACACAGATGCCAGC-----CTTAACTCAACTGGACAA----- 1413
QY      485 yProArgValTrpTyrArgProIleProSerHisMetProSerLeuHisAsnIleProVa 505
Db      1414 -----CCAAGT-----CCTGG 1424
QY      505 lProGluThrAsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuProProTh 525
Db      1425 ACCCCGAGGAGATCAGGGGCTGAGAGACAAAGCATGAATGCTCTCCGACGACCCGGA 1484
QY      525 RasPgluSerIleLys-----TyrThrIleTyrAsnSerThrGlyIleGlnI 541
Db      1485 GCCAAATCCAGTAAACAGGCGGACCGCTGCTTAACATATACACTGCTGCGGGTCAAGT 1544
QY      541 eGlyAlaTyrAsnTyrMetGluIleGlyGlyThrSerSer 554
Db      1545 TGGAGACACAACTACTTGAATGCAACAGACACTGCC 1584
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Search completed: June 25, 2003, 20:49:20